

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43; Search time 9.5 Seconds  
(without alignments)  
121.505 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIOLMNLG 12

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR 78:1\*  
2: PIR1:1\*  
3: PIR2:1\*  
4: PIR3:1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	35.6	12	2 S21205	Ig heavy chain V r
2	18	30.5	7	2 A58718	carnocin UI49 - Ca
3	18	30.5	9	2 S78420	ribosomal protein
4	18	30.5	10	2 A60589	sperm-activating p
5	18	30.5	10	2 B46453	e antigen p20e pre
6	17	28.8	7	2 I46868	alpha-myosin heavy
7	17	28.8	10	2 S28055	cytochrome b559 co
8	17	28.8	10	2 A37268	Ig heavy chain C r
9	16	27.1	9	2 S33636	coat protein beta
10	16	27.1	10	2 A47364	placental lactogen
11	15	25.4	7	2 S25265	p11f protein - Esc
12	15	25.4	7	2 S29735	polynephosphate-gluc
13	15	25.4	9	2 PWO002	Chlorophyll a/b-b1
14	15	25.4	9	2 A56029	N-methylpurine DNA
15	15	25.4	10	2 S27873	hypothetical prote
16	15	25.4	11	2 A38841	rhodopsin homolog
17	15	25.4	11	2 S35490	type II site-speci
18	15	25.4	11	2 B41935	translation elonga
19	15	25.4	11	2 A40795	glycoprotein H-a
20	15	25.4	12	2 A55837	5-aminomidazole r
21	14	23.7	4	2 I18888	COI inton 16 prot
22	14	23.7	7	2 UN0859	peptidyl-dipeptida
23	14	23.7	7	2 T09512	NADH2 dehydrogenas
24	14	23.7	9	2 PT0238	Ig heavy chain CRD
25	14	23.7	10	1 SPPGNK	neuroedin K - pig
26	14	23.7	10	2 C61033	renatechkinin C-
27	14	23.7	11	2 A55149	tetracenomycin A2
28	14	23.7	11	2 S60354	retinal oxidase -
29	14	23.7	11	2 B29806	acidic proline-ric

30	14	23.7	11	2 PH0904	T-cell receptor be
31	14	23.7	11	2 PH0924	T-cell receptor be
32	14	23.7	11	2 S41909	hypothetical prote
33	14	23.7	12	2 S25485	transcription fact
34	14	23.7	12	2 G49410	t-complex polypept
35	14	23.7	12	2 S71034	potB protein - Sal
36	14	23.7	12	2 C60529	hemocyanin 1 - gre
37	14	23.7	12	2 PH1180	T-cell receptor al
38	14	23.7	12	2 PH1187	T-cell receptor al
39	14	23.7	12	2 PH1189	T-cell receptor al
40	14	23.7	12	2 I41235	glutamine-tRNA lig
41	13	22.0	6	2 A20186	fatty-acid synthas
42	13	22.0	8	2 T14906	hypothetical prote
43	13	22.0	8	2 J50316	leucokinin VI - Ma
44	13	22.0	8	2 PH1618	Ig H chain V-D-J r
45	13	22.0	9	2 UN0026	sperm-activating p

## ALIGNMENTS

RESULT 1  
S21205  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S21205  
R:Makiya, R.; StriBrand, T.  
Eur. J. Biochem. 205, 341-345, 1992  
A>Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin.  
A:Reference number: S21205; PMID:92209522; PMID:1355892  
A:Accession: S21205  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <MA>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.6%; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 6.5e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQLMNLG 12  
DB 1 EVQLVESGG 9

RESULT 2  
A58718  
carnocin UI49 - Carnobacterium sp. (fragment)  
C:Species: Carnobacterium sp.  
C:Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C:Accession: A58718  
R:Stoffels, G.; Nissen-Meyer, U.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.  
Appl. Environ. Microbiol. 58, 1417-1422, 1992  
A>Title: Purification and characterization of a new bacteriocin isolated from a Carnoba  
A:Reference number: A58718; PMID:92321768; PMID:1622206  
A:Accession: A58718  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <STO>  
C:Keywords: antibiotic; lantionine

Query Match 30.5%; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6  
DB 2 SEIQ 5

RESULT 3  
S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
 C/Accession: S78420  
 R/Goldsmith-Reisin, S.; Graack, H.R.  
 submitted to the Protein Sequence Database, February 1998  
 A/Reference number: S78411  
 A/Accession: S78420  
 A/Molecule type: protein  
 A/Residues: 1-9 <GOL>  
 A/Note: the protein is designated as mitochondrial ribosomal protein L41  
 C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match  
 Best Local Similarity 30.5%; Score 18; DB 2; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
 DB 5 HRLG 8

RESULT 4  
 A60589  
 sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi  
 C/Species: Heterocentrotus mamillatus  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C/Accession: A60589  
 R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptidase  
 A/Reference number: A60527  
 A/Accession: A60589  
 A/Molecule type: protein  
 A/Residues: 1-10 <YOS>  
 C/Superfamily: unassigned animal peptides

Query Match  
 Best Local Similarity 30.5%; Score 18; DB 2; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12  
 DB 2 YNLG 5

RESULT 5  
 B46453  
 e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)  
 N/Alternate names: HBe antigen precursor  
 N/Contains: e antigen  
 C/Species: hepatitis B virus, HBV  
 A/Variety: subtype adr  
 C/Date: 18-Jun-1993 #sequence\_revision 08-Nov-1996 #text\_change 15-Aug-1997  
 C/Accession: B46453  
 R/Takahashi, K.; Kishimoto, S.; Otori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda, J.  
 J. Immunol. 147, 3156-3160, 1991  
 A/Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatitis B  
 A/Reference number: A46453; MUID:92013147; PMID:1717588  
 A/Accession: B46453  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <TK>  
 A/Experimental source: subtype adr  
 A/Note: sequence extracted from NCBI backbone (NCBIP:60243)  
 F/1-10/Domain: signal sequence (fragment) #status predicted <SIG>

Query Match  
 Best Local Similarity 30.5%; Score 18; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IQLMH 9

DB 1 IQLFH 5

RESULT 6  
 146868  
 alpha-myosin heavy chain - rabbit (fragment)  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
 C/Accession: 146868  
 R/Friedman, D.O.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
 A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular myosin heavy chain  
 A/Reference number: 146868; MUID:84221901; PMID:6328491  
 A/Accession: 146868  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-7 <FRI>  
 A/Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

Query Match  
 Best Local Similarity 28.8%; Score 17; DB 2; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMN 10  
 DB 1 QXMD 5

RESULT 7  
 S28055  
 cytochrome b559 component p6bf - pepper chloroplast (fragment)  
 C/Species: Chloroplast Capsicum annuum (pepper)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999  
 C/Accession: S28055  
 R/Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.  
 Plant Mol. Biol. 20, 1185-1188, 1992  
 A/Title: The p6bf gene from bell pepper (Capsicum annuum): plastid RNA editing also occurs in the cytochrome b559 component  
 A/Reference number: S28055; MUID:53099270; PMID:1463853  
 A/Accession: S28055  
 A/Molecule type: DNA  
 A/Residues: 1-10 <KUN>  
 A/Cross-references: EMBL:X65570; NID:g14344; PIDN:CAA46539.1; PID:g415734  
 C/Genetics:  
 A/Genome: p6bf  
 A/Suprafamily: cytochrome b559 component F  
 C/Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match  
 Best Local Similarity 28.8%; Score 17; DB 2; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8  
 DB 1 SISAMQFI 8

RESULT 8  
 A37268  
 Ig heavy chain C region (129) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
 C/Accession: A37268  
 R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A/Title: Heavy and light chain variable region sequences and antibody properties of anti-CD45 monoclonal antibodies  
 A/Reference number: A37268; MUID:9117923; PMID:1706720  
 A/Accession: A37268  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-10 <RUF>

Query Match 28.8%; Score 17; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 3.1e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIOLMNLG 12  
| | | | |  
| | | | |  
Db 1 ESQSPFNVG 9

RESULT 9  
S13636  
coat protein beta chain, Golgi-derived - rabbit (fragment)  
N/Alternate names: beta-COP protein  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C/Accession: S13636  
R/Submitter: T. Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orcl, L.; Rothman, J.E.; Wiele  
Nature 349, 215-220, 1991  
A/Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to t  
A/Reference number: S13636; MUID:9101693; PMID:1898984  
A/Accession: S13636  
A/Molecule type: protein  
A/Residues: 1-9 <SER>  
A/Status: preliminary  
C/Superfamily: coatmer complex beta chain  
C/Keywords: Golgi apparatus; protein transport

Query Match 27.1%; Score 16; DB 2; Length 9;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8  
| | | | |  
| | | | |  
Db 1 SLGHPIIV 8

RESULT 10  
A47364  
placental lactogen-I precursor - mouse (fragment)  
C/Species: Mus sp. (mouse)  
C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C/Accession: A47364  
R/Submitter: M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.  
Mol. Endocrinol. 7, 181-188, 1993  
A/Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro  
A/Reference number: A47364; MUID:9322595; PMID:8469232  
A/Accession: A47364  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-10 <RES>  
A/Cross-references: GB:S58124; NID:9259449

Query Match 27.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 4.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IOLMNL 11  
| | | | |  
| | | | |  
Db 1 MQLTLNL 7

RESULT 11  
S25266  
pIle protein - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 11-Jun-1993  
C/Accession: S25266  
R/Submitter: B.; Taha, M.K.; Possot, O.; Marchal, C.; Pugsley, A.P.  
Mol. Microbiol. 6, 1867-1894, 1992  
A/Title: Pilo, a component of the pullulanase secretion pathway of Klebsiella oxytoca, c  
A/Reference number: S25266; MUID:92374839; PMID:1354833  
A/Accession: S25266  
A/Molecule type: protein  
A/Residues: 1-7 <DUP>

C/Genetics:  
A/Genes: pIle  
Query Match 25.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IOLM 8  
| | | | |  
| | | | |  
Db 4 IELM 7

RESULT 12  
S29735  
poliphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi  
C/Species: Propionibacterium freudenreichi subsp. shermanii  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
C/Accession: S29735  
R/Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A/Title: The poliphosphate- and ATP-dependent glucokinase from Propionibacterium sherman  
A/Reference number: S29735; MUID:93143332; PMID:8380966  
A/Accession: S29735  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <PHI>  
C/Keywords: phosphotransferase

Query Match 25.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
| | | | |  
| | | | |  
Db 2 HVLG 5

RESULT 13  
PM0002  
chlorophyll a/b-binding protein 31k - green alga (Dunaliella tertiolecta) (fragment)  
N/Alternate names: photosystem II light-harvesting chlorophyll 31k protein  
C/Species: Dunaliella tertiolecta  
C/Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999  
C/Accession: PM0002  
R/Laroche, J.; Bennett, J.; Falkowski, P.C.  
Gene 95, 165-171, 1990  
A/Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the  
A/Reference number: J00040; MUID:91065528; PMID:224775  
A/Accession: PM0002  
A/Molecule type: protein  
A/Residues: 1-9 <LAR>  
C/Superfamily: chlorophyll a/b-binding protein  
C/Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane p

Query Match 25.4%; Score 15; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIOLM 8  
| | | | |  
| | | | |  
Db 5 EMOAM 9

RESULT 14  
A56029  
N-methylpurine DNA glycosylase - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 19-Jan-1996  
C/Accession: A56029  
R/Roy, R.; Brooks, C.; Mitra, S.  
Biochemistry 33, 15131-15140, 1994  
A/Title: Purification and biochemical characterization of recombinant N-methylpurine-DN  
A/Reference number: A56029; MUID:95092772; PMID:7999773

A/Accession: A56029  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-9 <ROY>

Query Match 25.4%; Score 15; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
 | : |  
 3 HEVG 6

## RESULT 15

S27873  
 hypothetical protein 2 LRH-1 5'-region - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C/Accession: S27873  
 R/Tugwood, J.D.; Issemann, I.; Green, S.  
 submitted to the EMBL Data Library, February 1992  
 A/Description: LRH-1: A nuclear hormone receptor active in the absence of exogenous liga  
 A/Reference number: S27873  
 A/Accession: S27873  
 A/Molecule type: mRNA  
 A/Residues: 1-10 <TUG>  
 A/Cross-references: EMBL:M81385; NID:G198872; PIDN:AAA39446.1; PID:G198874  
 C/Superfamily: unassigned leader peptides

Query Match 25.4%; Score 15; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 7.6e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQ 6  
 : : : : :  
 Db 5 NLSHIQ 10

Search completed: September 5, 2004, 09:37:43  
 Job time : 10.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds  
(without alignments)  
96.130 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQLMHNLG 12  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 501  
Minimum DB seq length: 0  
Maximum DB seq length: 12  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	30.5	7	1 LANC_CARUI	P36960 carnobacter
2	17	28.8	10	1 PSBF_CAPAN	Q03367 capsicum an
3	16	27.1	8	1 ALLC_CXDPO	P82157 cydia pomon
4	16	27.1	10	1 FUSF_FUSSO	P81010 fusarium so
5	16	27.1	10	1 RRPL_PHODV	P35946 phocine dis
6	16	27.1	11	1 EFG_CLOFA	P81350 clostridium
7	15	25.4	11	1 PVKI_PERAM	P41837 periplaneta
8	15	25.4	11	1 T2PI_PROVU	P31031 proteus vul
9	14	23.7	6	1 TRPI_PSEPU	P36414 pseudomonas
10	14	23.7	7	1 ALLC_CXDPO	P82158 cydia pomon
11	14	23.7	8	1 ALI8_CARMA	P81821 carcinus ma
12	14	23.7	8	1 ALLC_CXDPO	P82152 cydia pomon
13	14	23.7	9	1 FAR8_MACRS	P83281 macrobrachi
14	14	23.7	9	1 UF02_MOUSE	P38640 mus musculu
15	14	23.7	10	1 ALI9_CARMA	P81822 carcinus ma
16	14	23.7	10	1 TEMK_RANTE	P56923 rana tempor
17	14	23.7	10	1 TRNC_RANCA	P22890 rana catesb
18	14	23.7	10	1 TRNC_PIG	P01292 sus scrofa
19	14	23.7	11	1 ASLI_BACSE	P83146 bacteroides
20	14	23.7	12	1 CD11_LITXA	P56245 litoria xan
21	14	23.7	12	1 CD14_LITXA	P56246 litoria xan
22	14	23.7	12	1 HCVI_CARMA	P83176 carcinus ma
23	14	23.7	12	1 FORD_METHM	P80303 methanobact
24	14	23.7	12	1 RS19_TOBBP	Q56251 tomato big
25	13	22.0	8	1 LCK4_LEUMA	P21143 leucophaea
26	13	22.0	8	1 LCK6_LEUMA	P19988 leucophaea
27	13	22.0	9	1 MOSH_CLYJA	P19852 clypeaster
28	13	22.0	9	1 PPK1_PERAM	P82691 periplaneta
29	13	22.0	11	1 CSI5_BACSU	P81095 bacillus su
30	13	22.0	11	1 Q20A_COMTE	P80464 comamonas t
31	13	22.0	12	1 FA2B_VIPBO	P31859 vipera beru
32	13	22.0	12	1 PPK4_PERFU	P82690 periplaneta
33	13	22.0	12	1 UR2_POLSP	P81022 polyodon sp

ALIGNMENTS

RESULT 1

LANC\_CARUI STANDARD; PRT; 7 AA.  
ID LANC\_CARUI  
AC P36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
CX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H., Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SEIQ 6  
Db 2 SEIQ 5

RESULT 2

PSBF\_CAPAN STANDARD; PRT; 10 AA.  
ID PSBF\_CAPAN  
AC Q03367;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI (Fragment)).  
GN PSBF.  
OS Capsicum annuum (Bell pepper).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.  
OX NCBI\_TaxID=4072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;  
RX MEDLINE=93099270; PubMed=1463853;  
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;

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RT RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RL editing also occurs in non-photosynthetic chromoplasts."
CC CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC CC reaction center of photosystem II and possibly is part of the
CC CC water-oxidation complex.
CC CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC CC -!- SIMILARITY: Belongs to the psbE / psbF family.
CC CC -----
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL; X65570; CAA4539.1; -
DR DR PIR; S28055; S28055.
DR DR HAMAP; MF 00643; -; 1.
DR DR InterPro; IPR006216; Cyt b559.
DR DR PROSITE; PS00537; CYTOCHROME B559; PARTIAL.
KW KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT FT NON_TER 1 1
FT TRANSMEM <1 5 BY SIMILARITY.
FT DOMAIN 6 10 LUMENAL (POTENTIAL).
SQ SEQUENCE 10 AA; 1180 MW; 817D0F5D6D69DC5 CRC64;

Query Match 28.8%; Score 17; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.9e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQLM 8
Db 1 SISAMQFI 8

RESULT 3
ALL6_CYPDO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=932829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MNVLG 12
Db 3 LYNFG 7

RESULT 4

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FUSS_FUSSO STANDARD; PRT; 8 AA.
ID FUSS_FUSSO
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s 13596* (Fragment)
OS Fusarium solani (subsp. pisi) (Nectria haematococca);
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 27.1%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMHNL 11
Db 3 MSHNV 7

RESULT 5
RRPL_PHODV STANDARD; PRT; 10 AA.
ID RRPL_PHODV
AC P35946;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster/88;
RX MEDLINE=92268877; PubMed=1588321;
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
RT and sequence of the gene encoding the attachment (H) protein.";
RL J. Gen. Virol. 73:1189-1194(1992).
CC -!- FUNCTION: Probable component of the active polymerase. It may
CC function in mRNA synthesis, capping, methylation and poly(A)
CC synthesis of newly synthesized viral mRNAs, RNA editing of the p
CC gene transcript, and protein kinase activity.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -----
CC -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR DR EMBL; D10371; BAA01208.1; -
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;

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Query Match      27.1%; Score 16; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 0; Gaps 0;

QY 1 SVSEIOLM 8
    |||
Db 3 SVSVNQIL 10

RESULT 6
EFG CLOPA
ID _BFG CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
CX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RA MEDLINE=98291870; PubMed=9629918;
RX Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC -!- SIMILARITY: Belongs to the EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
KW PROSITE; PS00301; EFATOR GTP; PARTIAL.
DR Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match      27.1%; Score 16; DB 1; Length 11;
Best Local Similarity 25.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 IOLMHNLG 12
    :|:|:|
Db 4 LEKFNQIG 11

RESULT 7
PVK1 PERAM
ID _PVK1 PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
CX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=9523202; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
perisymphathetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
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CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match      25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IQLMHN 10
    |::|
Db 6 IFVNRN 11

RESULT 8
TZP1 PROVU
ID _TZP1 PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme Pvul (EC 3.1.21.4) (Endonuclease PvulI)
DE (R.PvulI) (Fragment).
GN PVUIR.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
CX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvulI restriction and
modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
CC EMBL; L04163; AAA25660.1; -
DR FIR; S35490; S35490.
DR REBASE; 1541; PvulI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match      25.4%; Score 15; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEI 5
    |||
Db 2 SVDEL 6

RESULT 9
TRPI PSEPU
ID _TRPI PSEPU STANDARD; PRT; 6 AA.
AC P36474;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
```

activator) (Fragment).

GN TRPI.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

CC Pseudomonadaceae; Pseudomonas.

OX NCBI\_TaxID=303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PPG1 C1S;

RX MEDLINE=89335826; PubMed=2503057;

RA Eberly L., Crawford I.P.;

RT "DNA sequence of the tryptophan synthase genes of Pseudomonas putida.";

RL Biochimie 71:521-531(1989).

CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

CC -!- SIMILARITY: Contains 1 HTH lysr-type DNA-binding domain.

CC -----

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CC -----

DR EMBL; X13299; CAA31660.1; --

DR InterPro; IPR000847; HTH Lysr.

DR PROSITE; PS50931; HTH\_LYSR; PARTIAL

KW Tryptophan biosynthesis; Transcription regulation; Activator;

KW DNA-binding.

FT NON TER

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds  
(without alignments)  
137.681 Million cell updates/sec

Title: US-09-730-174A-3

Perfect score: 59  
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp Vertebrate.\*  
14: sp\_unklassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	45.8	11	13	Q9PS71 agkistrodon
2	23	39.0	12	13	P82081 limnodynast
3	20	33.9	8	13	P82082 limnodynast
4	20	33.9	8	13	P82083 limnodynast
5	20	33.9	12	13	P82085 limnodynast
6	19	32.2	8	8	Q34909 locusta mig
7	19	32.2	9	12	O92766 canine dist
8	19	32.2	9	12	O71066 canine dist
9	18	30.5	8	10	Q40659 oryza sativ
10	18	30.5	10	12	Q9PXC3 hepatitis b
11	18	30.5	11	5	Q23876 dictyostell
12	18	30.5	12	15	Q85631 avian carc
13	17	28.8	7	6	Q28742 cryptolagus
14	17	28.8	9	4	Q15891 homo sapien
15	17	28.8	9	8	Q9GDI2 linoapadix
16	17	28.8	9	8	Q9GCV6 sclerosperm

Q35374 paramecium  
P82336 pisum sativ  
Q9PST1 fugu rubrip  
Q8J320 gallus gall  
Q05403 saccharomyc  
Q15894 homo sapien  
Q44377 aeromonas t  
Q44466 aeromonas v  
Q8RKU3 borrelia bu  
Q43928 aeromonas p  
Q44001 aeromonas e  
Q9K4M6 staphylococ  
Q9FXL0 lilium long  
Q7WUCL pseudomonas  
P82080 limnodynast  
Q66205 transmissib  
P82079 limnodynast  
Q43960 azotobacter  
Q8WTI9 drosophila  
Q8TS43 sus scrofa  
Q8WB77 chaitophoru  
Q61807 mus musculu  
Q9BDC8 pongo pygma  
Q9BDC9 gorilla gor  
Q9BDD0 pan troglod  
Q9BDC9 pan paniscu  
Q9K6Y0 aquifex pyr  
Q9TDY5 bos taurus  
Q47273 escherichia

17 17 28.8 11 8 Q35374  
18 17 28.8 11 10 P82336  
19 17 28.8 11 13 Q9PST1  
20 16 27.1 7 13 Q8J320  
21 16 27.1 8 3 Q05403  
22 16 27.1 8 4 Q15894  
23 16 27.1 9 2 Q44377  
24 16 27.1 9 2 Q44466  
25 16 27.1 9 2 Q8RKU3  
26 16 27.1 9 2 Q43928  
27 16 27.1 9 2 Q44001  
28 16 27.1 9 2 Q9K4M6  
29 16 27.1 9 10 Q9FXL0  
30 16 27.1 10 2 Q7WUCL  
31 16 27.1 10 13 P82080  
32 15 25.4 7 12 Q66205  
33 15 25.4 8 13 P82079  
34 15 25.4 9 2 Q43960  
35 15 25.4 9 5 Q8WTI9  
36 15 25.4 10 6 Q8TS43  
37 15 25.4 10 8 Q8WB77  
38 15 25.4 10 11 Q61807  
39 15 25.4 11 6 Q9BDC8  
40 15 25.4 11 6 Q9BDC9  
41 15 25.4 11 6 Q9BDD0  
42 15 25.4 11 6 Q9BDC9  
43 15 25.4 12 2 Q9K6Y0  
44 15 25.4 12 6 Q9TDY5  
45 14 23.7 8 2 Q47273

## ALIGNMENTS

RESULT 1

Q9PS71 PRELIMINARY; PRT; 11 AA.  
AC Q9PS71;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Fibrinolytic metalloproteinase (Fragment).  
OS Agkistrodon contortrix.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
OC Viperidae; Crotalinae; Agkistrodon.  
OX NCBI\_TaxID=8720;  
RN [1]  
RP MEDLINE=91378546; PubMed=1898066;  
RA Guan A.L., Retzius A.D., Henderson G.N., Markland P.S.Jr.;  
RT "Purification and characterization of a fibrinolytic enzyme from venom  
RT of the southern copperhead snake (Agkistrodon contortrix  
RL Arch. Biochem. Biophys. 289:197-207(1991).  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 45.8%; Score 27; DB 13; Length 11;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QLMHNLG 12  
: |||||  
Db 4 ELGHNLG 10

RESULT 2

P82081 PRELIMINARY; PRT; 12 AA.  
ID P82081  
AC P82081;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 3.  
 OS Limnodynastes terraereginae (Northern banjo frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OX NCBI\_TaxID=104894;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=TIBIAL GLAND;  
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 RT the banjo frogs Limnodynastes interioris, Limnodynastes dumerilii and  
 RT Limnodynastes terraereginae."  
 RL Aust. J. Chem. 46:833-842(1993).  
 CC -!- MASS SPECTROMETRY: MW=1236; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70DF472724 CRC64;  
  
 Query Match 39.0%; Score 23; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 1e+03; Indels 0; Gaps 0;  
 Matches 4; Conservative 2; Mismatches 0;  
  
 Qy 7 LMHNLG 12  
 Db 6 LLNLG 11  
  
 RESULT 3  
 P82082 ID P82082 PRELIMINARY; PRT; 8 AA.  
 AC P82082;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 4.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OX NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -!- MASS SPECTROMETRY: MW=772; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;  
  
 Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06; Indels 1; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 1;  
  
 Qy 7 LMHNLG 12  
 Db 2 LVSNLG 7  
  
 RESULT 4  
 P82083 ID P82083 PRELIMINARY; PRT; 8 AA.  
 AC P82083;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 5.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OX NCBI\_TaxID=39404;  
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -!- MASS SPECTROMETRY: MW=786; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;  
  
 Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 1;  
  
 Qy 7 LMHNLG 12  
 Db 2 LVSNLG 7  
  
 RESULT 5  
 P82085 ID P82085 PRELIMINARY; PRT; 12 AA.  
 AC P82085;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 7.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OX NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -!- MASS SPECTROMETRY: MW=1114; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;  
  
 Query Match 33.9%; Score 20; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 4.3e+03; Indels 1; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 1;  
  
 Qy 7 LMHNLG 12  
 Db 6 LVTNLG 11  
  
 RESULT 6  
 Q34909 ID Q34909 PRELIMINARY; PRT; 8 AA.  
 AC Q34909;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Locusta migratoria (Migratory locust).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=88223478; PubMed=2836084;  
 RA McCracken A., Ulenbusch I., Gellissen G.;  
 RT "Structure of the cloned Locusta migratoria mitochondrial genome:  
 RT restriction mapping and sequence of its ND-1 (ORF-1) gene."  
 RL Curr. Genet. 11:625-630(1987).  
 DR EMBL; X05286; CAA28905.1;  
 DR GO; GO:0005739; C:mitochondrion; IEA.

```
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8533723304B45B6 CRC64;

Query Match
Best Local Similarity 32.2%; Score 19; DB 8; Length 8;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMH 9
Db 1 MSYIKLKH 8

RESULT 7
O92766 PRELIMINARY; PRT; 9 AA.
AC O92766;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Alpha-amylase (Fragment).
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL EMBL; AF026237; AAC09167.1; -
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
FT NON_TER 9
FT SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match
Best Local Similarity 32.2%; Score 19; DB 12; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
Db 1 MHN 3

RESULT 8
O71066 PRELIMINARY; PRT; 9 AA.
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL EMBL; AF026234; AAC09164.1; -
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
FT NON_TER 9
FT SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

KW Query Match
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8533723304B45B6 CRC64;

Query Match
Best Local Similarity 32.2%; Score 19; DB 8; Length 8;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMH 9
Db 1 MSYIKLKH 8

RESULT 7
O92766 PRELIMINARY; PRT; 9 AA.
AC O92766;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Alpha-amylase (Fragment).
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL EMBL; AF026237; AAC09167.1; -
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
FT NON_TER 9
FT SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match
Best Local Similarity 32.2%; Score 19; DB 12; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
Db 1 MHN 3

RESULT 8
O71066 PRELIMINARY; PRT; 10 AA.
AC O9PXC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE E antigen P20E (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE.
RX MEDLINE=92013147; PubMed=1717588;
RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA Ohnuma H., Tsuda F., Muneata E., Miyakawa Y., Mayumi M.;
RT "Molecular heterogeneity of e antigen polypeptides in sera from
RT carriers of hepatitis B virus."
RL J. Immunol. 147:3156-3160(1991).
RL PIR; B46453; B46453.
FT NON_TER 10
FT SEQUENCE 10 AA; 1238 MW; 485A6E3AE721E9C7 CRC64;

Query Match
Best Local Similarity 30.5%; Score 18; DB 12; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLMHN 11
Db 1 MQLNNM 7

RESULT 10
O9PXC3 PRELIMINARY; PRT; 10 AA.
AC O9PXC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE E antigen P20E (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE.
RX MEDLINE=92013147; PubMed=1717588;
RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA Ohnuma H., Tsuda F., Muneata E., Miyakawa Y., Mayumi M.;
RT "Molecular heterogeneity of e antigen polypeptides in sera from
RT carriers of hepatitis B virus."
RL J. Immunol. 147:3156-3160(1991).
RL PIR; B46453; B46453.
FT NON_TER 10
FT SEQUENCE 10 AA; 1238 MW; 485A6E3AE721E9C7 CRC64;

Query Match
Best Local Similarity 30.5%; Score 18; DB 12; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLMHN 9
Db 1 MQLNNM 7
```

```

Db 1 MQLFH 5
RESULT 11
Q23876 PRELIMINARY; PRT; 11 AA.
AC Q23876;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8226045; PubMed=6286214;
RA McKewen M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium."
EL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL; K02957; AAA33150.1; -.
DR EMBL; K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match 30.5%; Score 18; DB 5; Length 11;
Best Local Similarity 28.6%; Pred. No. 1e+04;
Matches 2; Conservative 4; Mismatches 1; Indels 1; Gaps 0;

Qy 4 EIQLMHN 10
Db 5 DVOALNN 11

RESULT 12
Q85631 PRELIMINARY; PRT; 12 AA.
AC Q85631;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MH2, proviral DNA, myc to 3' LTR (Fragment).
OS Avian carcinoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11958;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85033920; PubMed=6092695;
RA Sutcliffe P., Jansen H.W., Bister K., Rapp U.R.;
RT "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT elements with avian sarcoma viruses Y73 and SR-A."
RL J. Virol. 52:703-705(1984).
DR EMBL; K03100; AAA42388.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;

Query Match 30.5%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNL 11
Db 2 HNL 4

RESULT 13
Q28742 PRELIMINARY; PRT; 7 AA.
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-myosin heavy chain (Rabbit).
OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains."
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
DR PIR; I46888; I46868.
FT NON_TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1B69326B0 CRC64;

Query Match 28.8%; Score 17; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 QLMEN 10
Db 1 QRMHD 5

RESULT 14
Q15891 PRELIMINARY; PRT; 9 AA.
ID Q15891
AC Q15891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP2E8B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32131; AAA73881.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1030 MW; E56635A1A33686D1 CRC64;

Query Match 28.8%; Score 17; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 EIQLMHNLG 12
Db 1 EHOMKTSLG 9

RESULT 15
QSGD12 PRELIMINARY; PRT; 9 AA.
ID QSGD12
AC QSGD12;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S16 (Fragment).
GN RPS16.
OS Lincspadix monostachya.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Arecaceae;

```

OC Areceae; Liospadicinae; Liospadix.  
OX NCBI\_TaxID=131282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Asmusen C.B., Chase M.W.;  
RT "Coding and noncoding plastid DNA in palm systematics."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ404941; CAC17917.1; -.  
DR GO; GO:0009507; Chloroplast; IEA.  
KW Chloroplast.  
FT NON TER 1 1  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1106 MW; 1B9236C2C0441B50 CRC64;  
  
Query Match 28.8%; Score 17; DB 8; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 IQLM 8  
Db 6 VQLM 9  
  
Search completed: September 5, 2004, 09:36:59  
Job time : 29.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds  
(without alignments)  
92.892 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQLMHNIG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1950s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	84.7	11	3 AAY96968	Aay96968 Parathyro
2	50	84.7	11	6 ABG72607	Abg72607 Parathyro
3	50	84.7	12	6 ABG72608	Abg72608 Parathyro
4	49	83.1	10	2 AAR91644	Aar91644 Human par
5	49	83.1	10	3 AAY68767	Aay68767 Amino aci
6	49	83.1	10	4 AAB86219	Aab86219 Human par
7	49	83.1	10	6 ABR44166	Abr44166 Human par
8	45	76.3	9	4 AAB86225	Aab86225 Human par
9	43	72.9	9	2 AAR91645	Aar91645 Human par
10	43	72.9	9	3 AAY96981	Aay96981 Parathyro
11	43	72.9	9	4 AAB86220	Aab86220 Human par
12	40.5	68.6	11	2 AAY50600	Aay50600 Resin bou
13	40	67.8	9	3 AAB01862	Aab01862 PTH(1-14)
14	40	67.8	9	3 AAY96966	Aay96966 Parathyro
15	37	62.7	9	3 AAB01863	Aab01863 PTH(1-14)
16	37	62.7	10	4 AAB86932	Aab86932 Rat parat
17	37	62.7	11	4 AAB86931	Aab86931 Rat parat
18	37	62.7	11	4 AAB86915	Aab86915 Parathyro
19	37	62.7	11	4 AAB84770	Aab84770 Parathyro
20	37	62.7	12	4 AAB86914	Aab86914 Parathyro
21	37	62.7	12	4 AAB84769	Aab84769 Parathyro
22	36	61.0	8	3 AAY78849	Aay78849 Parathyro
23	35	59.3	9	2 AAR91646	Aar91646 Human par
24	35	59.3	8	3 AAB07467	Aab07467 Antigenic
25	35	59.3	8	4 AAB86221	Aab86221 Human par

26	35	59.3	10	6 ABP71484	Abp71484 Parathyro
27	35	59.3	11	6 ABP71485	Abp71485 Parathyro
28	35	59.3	11	6 ABP71483	Abp71483 Parathyro
29	35	59.3	12	2 AA45785	Aa45785 Parathyro
30	35	59.3	12	6 ABP71482	Abp71482 Parathyro
31	33	55.9	9	3 AAB01866	Aab01866 PTH(1-14)
32	32	54.2	11	1 AAB82547	Aab82547 (Asn10, T
33	32	54.2	11	4 AAB86892	Aab86892 Rat parat
34	32	54.2	12	4 AAB96891	Aab96891 Rat parat
35	30	50.8	7	2 AAR91647	Aar91647 Human par
36	30	50.8	7	4 AAB86222	Aab86222 Human par
37	30	50.8	9	3 AAB01864	Aab01864 PTH(1-14)
38	30	50.8	9	3 AAY97062	Aay97062 PTH-rp N-
39	29	49.2	10	5 ABG69386	Abg69386 Vascular
40	29	49.2	12	5 AAR93357	Aar93357 Granulocy
41	27	45.8	11	4 ABUS4029	Abu54029 Human DNA
42	27	45.8	12	2 AAR89301	Aar89301 Japanese
43	27	45.8	12	3 AAB21270	Aab21270 Fertilin
44	26	44.1	6	2 AAR91648	Aar91648 Human par
45	26	44.1	6	3 AAY68764	Aay68764 Amino aci

ALIGNMENTS

RESULT 1  
AAY96968  
ID AAY96968 standard; peptide; 11 AA.  
XX AC AAY96968;  
XX DT 31-OCT-2000 (first entry)  
XX DE Parathyroid hormone N-terminal signaling domain (residues 1-11).  
XX KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX OS Homo sapiens.  
XX PN WO200039278-A2.  
XX PD 06-JUL-2000.  
XX PF 30-DEC-1999; 99WO-US031108.  
XX PR 31-DEC-1998; 98US-0114577P.  
XX XX (GARD//) GARDELLA T J.  
XX (KRON//) KRONENBERG H M.  
XX (POTT//) POTTS J T.  
XX (JUEP//) JUEPPNER H.  
Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
WPI; 2000-452384/39.  
New compound comprising an amino terminal signaling functional domain  
linked to a carboxy-terminal binding portion of parathyroid hormone for  
treating mammalian conditions characterized by decreases in bone mass.  
Claim 4; Page 92; 119pp; English.  
Compounds of the structure or formula S-(L)-n-B, R 1-S-(L)-n-R or S-(L)-n  
-R, are new. S is an amino terminal signaling functional domain of  
parathyroid hormone (PTH); L is a linker molecule present n times (where  
n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
sequence. The new compounds are used for treating mammalian conditions  
characterized by decreases in bone mass, determining rates of bone  
reformation, bone resorption and/or bone remodeling, treating diseases  
and disorders associated with decreased tether1 activity, increasing CAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (Claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHRP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 XX SQ Sequence 11 AA;

Query Match 84.7%; Score 50; DB 3; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.012; Indels 0; Gaps 0;  
 Matches 10; Conservative 1; Mismatches 0;  
 OY 1 SVSEIQLMHNLL 11  
 Db 1 AVSEIQLMHNLL 11

RESULT 2  
 ABG72607  
 ID ABG72607 standard; peptide; 11 AA.

XX AC ABG72607;  
 XX DT 11-FEB-2003 (first entry)

XX DE Parathyroid hormone antigenic peptide 2-12.

XX KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
 XX KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Rattus sp.

XX OS Bos taurus.

XX OS Sus scrofa.

XX OS Canis familiaris.

XX PH Key Location/Qualifiers

FT Misc-difference 6 /label= Leu, Phe

XX US2002110871-A1.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHK/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX DR WPI; 2003-066685/06.

XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
 PT and isolation of antibodies having an affinity to it, useful for  
 PT determining bioactive PTH levels in serum, plasma and/or cell culture  
 PT media.

XX Claim 1; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
 CC formation and isolation of antibodies having an affinity to it, being  
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are; (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by

CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
 XX canine and bovine PTH  
 XX SQ Sequence 11 AA;

Query Match 84.7%; Score 50; DB 6; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.012; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 1;

OY 2 VSEIQLMHNLLG 12  
 Db 1 VSEIQLMHNLLG 11

RESULT 3  
 ABG72608

ID ABG72608 standard; peptide; 12 AA.

XX AC ABG72608;

XX DT 11-FEB-2003 (first entry)

XX DE Parathyroid hormone antigenic peptide 1-12.

XX KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
 XX KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Rattus sp.

XX OS Bos taurus.

XX OS Sus scrofa.

XX OS Canis familiaris.

XX PH Key Location/Qualifiers

FT Misc-difference 1 /label= Ser, Ala

FT Misc-difference 7

FT /label= Leu, Phe

XX US2002110871-A1.

XX PD 15-AUG-2002.

XX PF 05-DEC-2000; 2000US-00730174.

XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHK/) ZAHRADNIK R J.

XX PA (LAVI/) LAVIGNE J R.

XX PI Zahradnik RJ, Lavigne JR;

XX DR WPI; 2003-066685/06.

XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
 PT and isolation of antibodies having an affinity to it, useful for  
 PT determining bioactive PTH levels in serum, plasma and/or cell culture  
 PT media.  
 XX Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
 CC formation and isolation of antibodies having an affinity to it, being  
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are; (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH

XX Sequence 12 AA;

Query Match 84.7%; Score 50; DB 6; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLG 12

Db 2 VSEIQXMHNLG 12

RESULT 4

AAAR91644  
 ID AAR91644 standard; peptide; 10 AA.

XX AC AAR91644;

XX DT 06-NOV-1996 (first entry)

XX DE Human parathyroid hormone antigenic peptide hPTH 1-10.

XX KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 XX diagnosis; active hPTH 1-37.

XX OS Synthetic.

XX PN DE4434551-A1.

XX PD 04-APR-1996.

XX PF 28-SEP-1994; 94DE-04434551.

XX PR 28-SEP-1994; 94DE-04434551.

XX PA (FORS/) FORSMANN W.

XX PI Adermann K, Forssmann W, Hock D, Maegerlein M;

XX DR WPI; 1996-180391/19.

XX PT New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 XX generated using them, able to distinguish between active and inactive  
 XX forms of the hormone.

XX PS Claim 2; Page 4; 5pp; German.

XX

CC The present sequence is a specific example of claimed immunogenic  
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 CC terminal alpha-helical region and/or the non-structured region of the  
 CC hormone. Antibodies and their binding fragments generated by injecting an  
 CC animal with the peptides are useful as diagnostic reagents for  
 CC determination of biologically active hPTH(1-37)

SQ Sequence 10 AA;

Query Match 83.1%; Score 49; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHN 10

Db 1 SVSEIQLMHN 10

RESULT 5

AAAY68767  
 ID AAY68767 standard; peptide; 10 AA.

XX AC AAY68767;

XX DT 05-MAY-2000 (first entry)

XX DE Amino acids 1-10 of a parathyroid hormone (PTH).

XX KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
 XX slimming treatment; cellulite; skin firming.

XX OS Unidentified.

XX PN WO200004047-A1.

XX PD 27-JAN-2000.

XX PF 07-JUL-1999; 99WO-FR001687.

XX PR 17-JUL-1998; 98FR-00009193.

XX PA (SEDE-) SEDERMA.

XX PI Lintner K;

XX DR WPI; 2000-171243/15.

XX PT New parathyroid hormone fragment peptides, used as lipolysis scimitants  
 XX in topically applied cosmetic compositions for slimming treatment of  
 XX excessive weight in hips and thighs.

XX PS Claim 1; Page 8; 18pp; French.

XX CC The present sequence represents a parathyroid hormone (PTH) fragment,  
 XX comprising amino acids 1-10. Parathyroid hormone fragments of the  
 XX invention have lipolysis stimulating activity (especially when topically  
 XX administered). The lipolytic activity of the peptides is enhanced when  
 XX they are chemically modified to increase their lipophilicity. The  
 XX peptides are used in cosmetic or dermatological compositions for skin  
 XX care. They are especially used for slimming treatment of excessive weight  
 XX in the thighs and hips, in the treatment of cellulite and for skin  
 XX firming

SQ Sequence 10 AA;

Query Match 83.1%; Score 49; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHN 10

Db 1 SVSEIQLMHN 10

```

RESULT 6
AAB86219
ID AAB86219 standard; peptide; 10 AA.
XX
XX AAB86219;
AC
XX 03-SEP-2001 (first entry)
XX
XX Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX hypo-parathyroidism; hyper-parathyroidism.
XX
XX Homo sapiens.
XX
XX DE19961350-A1.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99DE-01061350.
XX
XX 17-DEC-1999; 99DE-01061350.
XX
XX (IMMU-) IMMUNDIAGNOSTIK AG.
XX
XX Ambruster FP;
XX
XX WPI; 2001-376318/40.
XX
XX Determining the content of physiologically active parathyroid hormone,
XX useful in diagnosis of calcium-metabolism disorders, using two antibodies
XX reactive with different epitopes.
XX
XX Disclosure; Page 3; 10pp; German.
XX
XX This invention describes a novel method for determining (M1) the content
XX of active parathyroid hormone (A) by treating a sample with (i) antibody
XX (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
XX and including the N-terminal residue and (ii) antibody (Ab2) that
XX recognizes an epitope within the receptor-binding site of (A). The number
XX of molecules that react with both antibodies is determined and used to
XX calculate the content of physiologically active (A). The method is used
XX for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
XX hyper-parathyroidism. The method (unlike known assays) recognizes that
XX (i) some fragments of (A) shorter than the complete (84 aa) peptide are
XX active and (ii) that apparently intact peptide may be biologically
XX inactive, and also takes into account the fact that some fragments of (A)
XX are antagonistic (these have the receptor-binding site but lack the N-
XX terminus). It thus provides a true measure of the content of
XX physiologically active (A); contrast methods that measure intact peptide
XX and its 1-37 fragment which may produce falsely high values. This
XX sequence represents a peptide fragment used to illustrate the method of
XX the invention
XX
XX Query Match 83.1%; Score 49; DB 4; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.017;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SVSEIQLMHN 10
XX | | | | |
XX Db 1 SVSEIQLMHN 10
XX
XX RESULT 7
XX ABR44166
XX ID ABR44166 standard; peptide; 10 AA.
XX
XX AC ABR44166;
XX
XX Query Match 83.1%; Score 49; DB 4; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.017;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SVSEIQLMHN 10
XX | | | | |
XX Db 1 SVSEIQLMHN 10
XX
XX RESULT 8
XX AAB86225
XX ID AAB86225 standard; peptide; 9 AA.
XX
XX AC AAB86225;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX hypo-parathyroidism; hyper-parathyroidism.
XX
XX Homo sapiens.
XX
XX DE19961350-A1.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99DE-01061350.
XX
XX

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DT 04-AUG-2003 (first entry)
XX
XX Human parathyroid hormone (hPTH) fragment (residues 1-10).
XX
XX Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
XX lipolysis; human; hPTH.
XX
XX Homo sapiens.
XX
XX WO2003035697-A1.
XX
XX 01-MAY-2003.
XX
XX 06-MAY-2002; 2002WO-KR000835.
XX
XX 27-SEP-2001; 2001KR-00060245.
XX
XX 15-MAR-2002; 2002KR-00014062.
XX
XX (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.
XX
XX Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;
XX Chang M;
XX
XX WPI; 2003-468288/44.
XX
XX Novel fusion peptide comprising self cell-penetrating tat peptide bound
XX to human parathyroid hormone-derived peptide, useful as component of skin
XX slimming cosmetic composition.
XX
XX Claim 5; Page 6; 32pp; English.
XX
XX The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
XX penetrating Tat peptide is bound to human parathyroid hormone-derived
XX peptide (hPTHDP). The fusion peptide is useful as a component of skin
XX slimming cosmetic composition. The fusion peptide does not cause
XX irritation, easily and safely penetrates into integument and endothelium,
XX does not cause skin disease and has superior lipolysis effects, and is
XX durable. The present sequence represents a human parathyroid hormone
XX (hPTH) fragment that can be used to construct the fusion peptide
XX
XX Sequence 10 AA;
XX
XX Query Match 83.1%; Score 49; DB 6; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.017;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 SVSEIQLMHN 10
XX | | | | |
XX Db 1 SVSEIQLMHN 10
XX
XX RESULT 8
XX AAB86225
XX ID AAB86225 standard; peptide; 9 AA.
XX
XX AC AAB86225;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
XX diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
XX hypo-parathyroidism; hyper-parathyroidism.
XX
XX Homo sapiens.
XX
XX DE19961350-A1.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99DE-01061350.
XX
XX

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PR 17-DEC-1999; 99DE-01061350.
XX (IMMU-) IMMUNDIAGNOSTIK AG.
XX Ambruster FP;
XX WPI; 2001-376318/40.
XX
XX Determining the content of physiologically active parathyroid hormone,
XX useful in diagnosis of calcium-metabolism disorders, using two antibodies
XX reactive with different epitopes.
XX
XX Disclosure; Page 3; 10pp; German.
XX
XX This invention describes a novel method for determining (M1) the content
XX of active parathyroid hormone (A) by treating a sample with (i) antibody
XX (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
XX and including the N-terminal residue and (ii) antibody (Ab2) that
XX recognizes an epitope within the receptor-binding site of (A). The number
XX of molecules that react with both antibodies is determined and used to
XX calculate the content of physiologically active (A). The method is used
XX for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
XX hyper-parathyroidism. The method (unlike known assays) recognizes that
XX (1) some fragments of (A) shorter than the complete (84 aa) peptide are
XX active and (ii) that apparently intact peptide may be biologically
XX inactive, and also takes into account the fact that some fragments of (A)
XX are antagonistic (these have the receptor-binding site but lack the N-
XX terminus). It thus provides a true measure of the content of
XX physiologically active (A); contrast methods that measure intact peptide
XX and its 1-37 fragment which may produce falsely high values. This
XX sequence represents a peptide fragment used to illustrate the method of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 76.3%; Score 45; DB 4; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 VSEIQLMHN 10
XX 1 VSEIQLMHN 9
XX
XX RESULT 9
XX AAR91645
XX ID AAR91645 standard; peptide; 9 AA.
XX AC
XX AAR91645;
XX DT 06-NOV-1996 (first entry)
XX
XX DE Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
XX diagnosis; active hPTH 1-37.
XX Synthetic.
XX DE4434551-AL.
XX
XX 04-APR-1996.
XX
XX 28-SEP-1994; 94DE-04434551.
XX
XX 28-SEP-1994; 94DE-04434551.
XX (FORS/) FORSMANN W.
XX
XX Adermann K, Forssmann W, Hock D, Maegerlein M;
XX WPI; 1996-180391/19.
XX
XX
XX New antigenic peptide(s) from human parathyroid hormone - and antibodies
XX generated using them, able to distinguish between active and inactive
XX forms of the hormone.
XX
XX Claim 2; Page 4; 5pp; German.
XX
XX The present sequence is a specific example of claimed immunogenic
XX peptides having a sequence from hPTH(1-37) which includes the N- or C-
XX terminal alpha-helical region and/or the non-structured region of the
XX hormone. Antibodies and their binding fragments generated by injecting an
XX animal with the peptides are useful as diagnostic reagents for
XX determination of biologically active hPTH(1-37)
XX
XX Sequence 9 AA;
XX
XX Query Match 72.9%; Score 43; DB 2; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SVSEIQLMHN 9
XX 1 SVSEIQLMHN 9
XX
XX RESULT 10
XX AAY96981
XX ID AAY96981 standard; peptide; 9 AA.
XX AC
XX AAY96981;
XX DT 31-OCT-2000 (first entry)
XX
XX DE Parathyroid hormone N-terminal signaling domain.
XX
XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
XX bone reformation; resorption; remodeling; tether1; osteoporosis.
XX Homo sapiens.
XX WC200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Claim 11; Page 93; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
XX PTH-1 receptor signal sequence; and R is a portion of PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing CAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or

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CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis

SQ Sequence 9 AA;

Query Match 72.9%; Score 43; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
 |||||  
 Db 1 SVSEIQLMH 9

RESULT 11  
 AAB86220  
 ID AAB86220 standard; peptide; 9 AA.

AC AAB86220;  
 DT 03-SEP-2001 (first entry)  
 XX Human parathyroid hormone immunogenic peptide SEQ ID 2.  
 DE  
 DE Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.

OS Homo sapiens.

XX DE19961350-A1.

PN 21-JUN-2001.

PD 17-DEC-1999; 99DE-01061350.

PP 17-DEC-1999; 99DE-01061350.

PR (IMMU-) IMMUNDIAGNOSTIK AG.

PA Armbruster FP;

PI WPI: 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.

XX Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention

SQ Sequence 9 AA;

Query Match 72.9%; Score 43; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMH 9  
 |||||  
 Db 1 SVSEIQLMH 9

RESULT 12

AAAY50600

ID AAAY50600 standard; peptide; 11 AA.

XX AC AAAY50600;

XX 09-FEB-2000 (first entry)

XX Resin bound cyclic peptide 33.

XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
 KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;  
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.  
 XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "FMOC-Ala"

FT Misc-difference 3 /note= "Ser(OtBu)"

FT Misc-difference 4 /note= "Glu(OtBu)"

FT Misc-difference 6 /note= "Gln(Trt)"

FT Misc-difference 9 /note= "His(Trt)"

FT Misc-difference 10 /note= "Asn(Trt)"

XX WO9952933-A1.

XX 21-OCT-1999.

XX 15-APR-1999; 99WO-US0008435.

XX 15-APR-1998; 98US-0081897P.

XX (RHON ) RHONE-POULENC RORER PHARM INC.

XX Sledeski AW, Mencil JJ;

XX WPI: 1999-633822/54.

XX Convergent synthesis of peptides for treating e.g. bone disorders.

XX Disclosure; Page 75; 85pp; English.

XX This invention describes a novel method for the preparation of peptides  
 CC (II) that contain both cyclic and linear peptide fragments comprises  
 CC sequential reaction of a resin-bound linear fragment with the cyclic  
 CC fragment in N-protected form and optionally other linear fragments. The  
 CC products of the invention have osteopathic and hypotensive activity. (II)  
 CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The  
 CC method is particularly used to prepare cyclic peptide analogs of  
 CC parathyroid hormone (PTH) or PTH-related peptides which are useful for  
 CC treating diseases that respond to treatment with agents that bind to PTH  
 CC receptors (with or without activation of adenylyl cyclase activity), e.g.  
 CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-  
 CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also  
 CC for promoting repair of bone fractures. Separate synthesis of the cyclic  
 CC fragment allows convergent synthesis of resin-bound (II), with better  
 CC yields and higher throughput. The difficulties associated with  
 CC preparation of the bridged fragment are confined to a small peptide which

CC can be purified before reaction with the resin-bound component. AAY50568-  
CC Y50614 represent the peptide fragments described in the method of the  
CC invention  
XX  
XX  
SQ Sequence 11 AA;  
  
Query Match 68.6%; Score 40.5; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 0.73;  
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 SVSEIQLMNLG 12  
DB :||||| |||||  
1 AVSEIQL-HNLG 11  
  
RESULT 13  
AAB01862  
ID AAB01862 standard; peptide; 9 AA.  
XX  
AC AAB01862;  
XX  
DT 11-SEP-2000 (first entry)  
XX  
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.  
XX  
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
XX calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200023594-A1.  
XX  
PD 27-APR-2000.  
XX  
PF 20-OCT-1999; 99WO-US024481.  
XX  
PR 22-OCT-1998; 98US-0105530P.  
XX  
PA (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-339693/29.  
XX  
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
PT acids that encode them, useful for treating osteoporosis.  
XX  
PS Disclosure; Page 26; 73pp; English.  
XX  
CC The invention relates to a novel parathyroid hormone (PTH) peptide  
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
CC B01869). The peptides of the invention are at least 85% identical to the  
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
CC provided that the peptide is not PTHrP(1-14). The peptides of the  
CC invention also encompass fragments of peptides of the invention  
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
CC and is necessary for the normal function of the gastrointestinal,  
CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
CC effect on the skeleton, and mediates calcium reabsorption, enhances  
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
CC the renal and skeletal actions of PTH, and also bind to the PTH-1

CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
CC conditions characterized by a decrease in bone mass, such as  
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
CC medical disorders that arise from excessive or altered action of the PTH-  
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
CC useful in the determination of rates of bone formation, bone resorption  
CC and/or bone remodelling in a patient. The peptides of the invention are  
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
CC conventional synthetic chemistry, and can be delivered to a patient via  
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
CC PTH-1/PTH-2 receptor agonists  
XX  
SQ Sequence 9 AA;  
  
Query Match 67.8%; Score 40; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVSEIQLMH 9  
DB :||||| |||||  
1 AVSEIQLMH 9  
  
RESULT 14  
AAY96966  
ID AAY96966 standard; peptide; 9 AA.  
XX  
AC AAY96966;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone N-terminal signaling domain (residues 1-9).  
XX  
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-US031108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
PA (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
XX  
DR New compound comprising an amino terminal signaling functional domain  
XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
XX treating mammalian conditions characterized by decreases in bone mass.  
XX  
PS Claim 4; Page 92; 119pp; English.  
XX  
CC Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
CC -R, are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether1 activity, increasing CAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 SQ Sequence 9 AA;

Query Match 67.8%; Score 40; DB 3; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYSEIQLMH 9  
 :|||||||  
 Db 1 AVSEIQLMH 9

RESULT 15  
 AAB01863  
 ID AAB01863 standard; peptide; 9 AA.

XX AAB01863;

DT 11-SEP-2000 (first entry)

DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.

XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 KW Calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.

OS Homo sapiens.  
 OS Synthetic.

PN WO200023594-A1.

XX 27-APR-2000.

PF 20-OCT-1999; 93WO-US024481.

PR 22-OCT-1998; 98US-0105530P.

PA (GARD/) GARDELLA T J.  
 PA (KRON/) KRONENBERG H M.  
 PA (POTT/) POTTS J T.  
 PA (JUEP/) JUEPPNER H.

PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-339693/29.

XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 PT acids that encode them, useful for treating osteoporosis.

PS Disclosure; Page 26; 73pp; English.

XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterised by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodelling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists

XX SQ Sequence 9 AA;

Query Match 62.7%; Score 37; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYSEIQLMH 9  
 :|||||||  
 Db 1 AVSEIQLMH 9

Search completed: September 5, 2004, 09:34:30  
 Job time : 38.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds  
(without alignments)  
116.332 Million cell updates/sec

Title: US-09-730-174A-3  
Perfect score: 59  
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 31505143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	12	9	US-09-730-174A-3
2	56	94.9	12	9	US-09-730-174A-5
3	55	93.2	11	9	US-09-730-174A-1
4	55	93.2	12	9	US-09-730-174A-4
5	52	88.1	11	9	US-09-730-174A-6
6	51	86.4	11	9	US-09-730-174A-2
7	49	83.1	10	14	US-10-168-185-1
8	45	76.3	9	14	US-10-168-185-7
9	43	72.9	9	14	US-10-168-185-2
10	41	69.5	8	14	US-10-168-185-8
11	40	67.8	9	14	US-10-168-185-6
12	37	62.7	8	14	US-10-192-673-6
13	35	59.3	8	14	US-10-192-673-7
14	33	55.9	9	14	US-10-168-185-3
15	30	50.8	7	14	US-10-192-673-10

16	30	50.8	9	14	US-10-192-673-8
17	29	49.2	10	14	US-10-033-741-61
18	28	47.5	9	9	US-09-746-945-6
19	28	47.5	12	14	US-10-319-130-16
20	27	45.8	11	16	US-10-391-364-93
21	26	44.1	6	14	US-10-168-185-5
22	25	44.1	10	14	US-10-168-185-11
23	25	42.4	11	12	US-09-747-287-185
24	25	42.4	11	12	US-09-874-350A-151
25	24	40.7	10	9	US-09-826-290-27
26	24	40.7	10	16	US-10-264-309-369
27	24	40.7	10	16	US-10-432-234A-75
28	24	40.7	10	16	US-10-432-234A-76
29	24	40.7	10	16	US-10-432-234A-77
30	24	40.7	11	12	US-10-609-217-41
31	24	40.7	11	12	US-10-632-388-41
32	24	40.7	11	12	US-10-651-723-41
33	24	40.7	11	12	US-10-645-761-41
34	24	40.7	11	16	US-10-668-696-41
35	24	40.7	11	16	US-10-653-048-41
36	24	40.7	12	14	US-10-286-457-294
37	23	39.0	7	14	US-10-286-457-469
38	23	39.0	7	15	US-10-368-280-12
39	23	39.0	7	15	US-10-374-035-12
40	23	39.0	9	9	US-09-894-018-332
41	23	39.0	9	10	US-09-821-734-4
42	23	39.0	9	10	US-09-854-248-11
43	23	39.0	9	12	US-10-253-286-288
44	23	39.0	9	14	US-10-094-699-50
45	23	39.0	9	15	US-10-117-937-249

ALIGNMENTS

RESULT 1

US-09-730-174A-3  
; Sequence 3, Application US/09730174A  
; Patent No. US2002110871A1  
; GENERAL INFORMATION:  
; APPLICANT: Zahradnik, R.J.  
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having ;  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H ;  
; FILE REFERENCE: IMUNE-001A  
; CURRENT APPLICATION NUMBER: US/09/730,174A  
; CURRENT FILING DATE: 2000-12-05  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 3  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-3

Query Match 100.0%; Score 59; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00081;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SVSEIQLMHNLG 12  
|||  
Db 1 SVSEIQLMHNLG 12

RESULT 2

US-09-730-174A-5  
; Sequence 5, Application US/09730174A  
; Patent No. US20020110871A1  
; GENERAL INFORMATION:  
; APPLICANT: Zahradnik, R.J.  
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having ;  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H ;  
; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 5  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-5

Query Match 94.9%; Score 56; DB 9; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.0027;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLG 12  
 :|||||  
 Db 1 AVSEIQFMHNLG 12

# RESULT 3

US-09-730-174A-1

; Sequence 1, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 1  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-1

Query Match 93.2%; Score 55; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0038;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLG 12  
 :|||||  
 Db 1 VSEIQLMHNLG 11

# RESULT 4

US-09-730-174A-4

; Sequence 4, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 4  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-4

Query Match 93.2%; Score 55; DB 9; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.0041;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLG 12  
 :|||||  
 Db 1 SVSEIQFMHNLG 12

# RESULT 5

US-09-730-174A-6

; Sequence 6, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 6  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-6

Query Match 88.1%; Score 52; DB 9; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 0.014;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLG 12  
 :|||||  
 Db 1 AVSEIQFMHNLG 12

# RESULT 6

US-09-730-174A-2

; Sequence 2, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-2

Query Match 86.4%; Score 51; DB 9; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.019;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLG 12  
 :|||||  
 Db 1 VSEIQFMHNLG 11

# RESULT 7

US-10-168-185-1

; Sequence 1, Application US/10168185  
 ; Publication No. US20030175802A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Armbruster, Franz Paul  
 ; APPLICANT: Missbichler, Albert  
 ; APPLICANT: Schmidt-Gayk, Heinrich  
 ; APPLICANT: Roth, Heinz-Jürgen  
 ; TITLE OF INVENTION: Method for Determining Parathormone

```
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-12-17
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 10
; ORGANISM: Homo sapiens
US-10-168-185-1

Query Match      83.1%; Score 49; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVSEIQLMHN 10
Db      1 SVSEIQLMHN 10

RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match      76.3%; Score 45; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VSEIQLMHN 10
Db      1 VSEIQLMHN 9

RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match      76.3%; Score 45; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VSEIQLMHN 10
Db      1 VSEIQLMHN 9

RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Homo sapiens
US-10-168-185-2

Query Match      72.9%; Score 43; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVSEIQLMHN 9
Db      1 SVSEIQLMHN 9

RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 8
; ORGANISM: Homo sapiens
US-10-168-185-8

Query Match      69.5%; Score 41; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SEIQLMHN 10
Db      1 SEIQLMHN 8

RESULT 11
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T.
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
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; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
; PRIOR FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-192-673-6

Query Match 67.8%; Score 40; DB 14; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.2e+06;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9  
Db 1 AVSEIQLMH 9

RESULT 12  
US-10-192-673-7  
; Sequence 7, Application US/10192673  
; Publication No. US20030166838A1  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald  
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
; FILE REFERENCE: 0609.4570002  
; CURRENT APPLICATION NUMBER: US/10/192,673  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: U.S. 09/421,379  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
; PRIOR FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-192-673-7

Query Match 62.7%; Score 37; DB 14; Length 9;  
Best Local Similarity 77.8%; Pred. No. 1.2e+06;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9  
Db 1 AVSEIQLMH 9

RESULT 13  
US-10-168-185-3  
; Sequence 3, Application US/10168185  
; Publication No. US20030175802A1  
; GENERAL INFORMATION:  
; APPLICANT: Armbruster, Franz Paul  
; APPLICANT: Missbichler, Albert  
; APPLICANT: Schmidt-Gayk, Heinrich  
; APPLICANT: Roth, Heinz-Jürgen  
; TITLE OF INVENTION: Method for Determining Parathormone  
; TITLE OF INVENTION: Activity in a Human Sample

; FILE REFERENCE: HLZ-004US  
; CURRENT APPLICATION NUMBER: US/10/168,185  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: DE 19961350  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-185-3

Query Match 59.3%; Score 35; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLM 8  
Db 1 SVSEIQLM 8

RESULT 14  
US-10-192-673-10  
; Sequence 10, Application US/10192673  
; Publication No. US20030166838A1  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald  
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
; FILE REFERENCE: 0609.4570002  
; CURRENT APPLICATION NUMBER: US/10/192,673  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: U.S. 09/421,379  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
; PRIOR FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-192-673-10

Query Match 55.9%; Score 33; DB 14; Length 9;  
Best Local Similarity 77.8%; Pred. No. 1.2e+06;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9  
Db 1 SVSEIQLMH 9

RESULT 15  
US-10-168-185-4  
; Sequence 4, Application US/10168185  
; Publication No. US20030175802A1  
; GENERAL INFORMATION:  
; APPLICANT: Armbruster, Franz Paul  
; APPLICANT: Missbichler, Albert  
; APPLICANT: Schmidt-Gayk, Heinrich  
; APPLICANT: Roth, Heinz-Jürgen  
; TITLE OF INVENTION: Method for Determining Parathormone

```

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-185-4

Query Match          50.8%; Score 30; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      ,      1 SVSEIQL 7
        |||||
Db      1 SVSEIQL 7

Search completed: September 5, 2004, 09:49:37
Job time : 33.5 secs

```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43 ; Search time 9.5 Seconds  
(without alignments)  
121.505 Million cell updates/sec

Title: US-09-730-174A-4

Perfect score: 61

Sequence: 1 SVSEIQFMHLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	37.7	10	2 S28055	cytochrome b559 co
2	18	29.5	7	2 A58718	carnocin UI49 - Ca
3	18	29.5	9	2 S78420	ribosomal protein
4	18	29.5	10	2 A60589	sperm-activating p
5	17	27.9	8	2 A05169	neuropeptide M-I
6	17	27.9	10	2 A37268	Ig heavy chain C r
7	17	27.9	12	2 S21205	Ig heavy chain v r
8	17	27.9	12	2 PH1187	T-cell receptor al
9	16	26.2	7	2 I46868	alpha-myosin heavy
10	16	26.2	9	2 G58502	kidney and bladder
11	16	26.2	10	2 JC1416	hypertrehalosemic
12	16	26.2	10	2 S09138	hypertrehalosemic
13	16	26.2	11	2 A34248	amine oxidase (cop
14	15	24.6	7	2 S29735	polymorphate-gluc
15	15	24.6	9	2 PT0231	Ig heavy chain CDR
16	15	24.6	9	2 A56029	N-methylpurine DNA
17	15	24.6	10	2 S33844	alpha-2-macroglobu
18	15	24.6	10	2 S37873	hypothetical prote
19	15	24.6	10	2 S28304	lectin GNL1 alpha
20	15	24.6	11	2 A38841	rhodopsin homolog
21	15	24.6	11	2 S35490	type II site-speci
22	15	24.6	12	2 PH1190	T-cell receptor al
23	15	24.6	12	2 S51737	T-cell receptor be
24	14	23.0	4	2 A35779	neuropeptide Antho
25	14	23.0	7	2 JN0859	peptidyl-dipeptida
26	14	23.0	7	2 S78024	ribosomal protein
27	14	23.0	8	2 S08995	hypertrehalosemic
28	14	23.0	8	2 A49823	adipokinetic hormo
29	14	23.0	8	2 A44960	neuropeptide led-C

chlorophyll a/b-bi  
coat protein beta  
Ig heavy chain CRD  
neuremedin K - pig  
ranatachykinin C -  
e antigen p20e pre  
nitrogenase (EC 1,  
translation elonga  
endo-i,4-beta-xyla  
protein QA300042 -  
retinal oxidase -  
beta-D-galactosida  
T-cell receptor be  
locustanmyotropin -  
transcription fact  
potS protein - Sal

#### ALIGNMENTS

##### RESULT 1

S28055  
cytochrome b559 component psbF - pepper chloroplast (fragment)  
C:Species: Chloroplast Capsicum annuum (pepper)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999  
C:Accession: S28055  
R:Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.  
Plant Mol. Biol. 20, 1185-1188, 1992  
A:Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occu  
A:Reference number: S28055; MUID:93099270; PMID:1463853  
A:Accession: S28055  
A:Molecule type: DNA  
A:Residues: 1-10 <KUN>  
A:Cross-references: EMBL:X65570; NID:gl4344; PIDN:CAA46539.1; PID:g415734  
C:Genetics:  
A:Gene: psbF  
A:Genome: chloroplast  
C:Superfamily: cytochrome b559 component F  
C:Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 37.7%; Score 23; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFM 8  
| : | : | : |  
Db 1 SISAMQFI 8

##### RESULT 2

A58718  
carnocin UI49 - Carnobacterium sp. (fragment)  
C:Species: Carnobacterium sp.  
C:Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C:Accession: A58718  
R:Stoffeis, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.  
Appl. Environ. Microbiol. 58, 1417-1422, 1992  
A:Title: Purification and characterization of a new bacteriocin isolated from a Carnoba  
A:Reference number: A58718; MUID:92321768; PMID:1622206  
A:Accession: A58718  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <SFO>  
C:Keywords: antibiotic; lanthionine

Query Match 29.5%; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6  
| : | : | : |  
Db 2 SEIQ 5



RESULT 9  
I46868  
alpha-myosin heavy chain - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
C:Accession: I46868  
R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
A:Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular myosin heavy chain  
A:Reference number: I46868, MUID:84221901, PMID:6328491  
A:Accession: I46868  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-7 <FRI>  
A:Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

Query Match 26.2%; Score 16; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMHN 10  
| : : :  
| : : :  
Db 1 QKQHD 5

RESULT 10  
G58502  
kidney and bladder stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C:Accession: G58502  
R:Binette, J.P.; Binette, M.B.  
Submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: G58502  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <BIN>  
A:Experimental source: human kidney stone, bladder stone  
A>Note: a secondary sequence AAKENPXD was also found

Query Match 26.2%; Score 16; DB 2; Length 9;  
Best Local Similarity 28.6%; Pred. No. 2.8e+05;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQF 7  
| : : :  
| : : :  
Db 1 SLPDVKF 7

RESULT 11  
JCL1416  
hypertrehalosemic hormone I - stick insect (Carausius morosus)  
N:Alternate names: neuropeptide Cam-HrTH-I  
N:Contains: hypertrehalosemic factor II  
C:Species: Carausius morosus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: JCL1416; S07157  
R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect  
A:Reference number: JCL1416; MUID:93129188; PMID:1482345  
A:Accession: JCL1416  
A:Molecule type: protein  
A:Residues: 1-10 <GAEI>  
R:Gaede, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A:Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacum of the stick insect Carausius morosus  
A:Reference number: S07157; MUID:87157103; PMID:3828078  
A:Accession: S07157

A:Molecule type: protein  
A:Residues: 'Z', 2-10 <GAE2>  
C:Comment: Hypertrehalosemic factor II lacks the tryptophan modification.  
C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplaneta americana.  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Binding site: carbohydrate (Tyr) (covalent) #status experimental  
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 4.8e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12  
| : : :  
| : : :  
Db 1 QLTFPNWG 9

RESULT 12  
S09138  
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)  
N:Alternate names: Cam-HrTH-II  
C:Species: Extatosoma tiaratum  
C:Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
C:Accession: S09138  
R:Gaede, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A:Reference number: S08995; MUID:90253659; PMID:2340112  
A:Accession: S09138  
A:Molecule type: protein  
A:Residues: 1-10 <GAB>  
A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have used the sequence GAB instead of the expected GAE.  
C:Superfamily: adipokinetic hormone  
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 4.8e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12  
| : : :  
| : : :  
Db 1 QLTFPNWG 9

RESULT 13  
A32428  
amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 12-Oct-1999 #sequence\_revision 31-Dec-1993 #text\_change 06-Sep-1996  
C:Accession: A32428  
R:van der Meer, R.A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A.  
Biochem. Biophys. Res. Commun. 159, 726-733, 1989  
A:Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolated from the liver of the pig  
A:Reference number: A32428; MUID:89193662; PMID:2539124  
A:Accession: A32428  
A:Molecule type: protein  
A:Residues: 1-7, 'K', 9-11 <VAN>  
A>Note: the modified residue thought by the authors to be pyrroloquinoline quinone covalently bound to the protein  
C:Keywords: oxidoreductase; quinoprotein; topaquinone  
F:8/Modified site: topaquinone (Tyr) #status predicted

Query Match 26.2%; Score 16; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 5.3e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 SEIQFMHN 10  
| : : :  
| : : :  
Db 2 SDAVFTYN 9

## RESULT 14

S29735  
 polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichii  
 C:Species: Propionibacterium freudenreichii subsp. shermanii  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
 C:Accession: S29735  
 R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
 Arch. Biochem. Biophys. 300, 309-319, 1993  
 A:Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium shermanii  
 A:Reference number: S29735; MUID:93143332; PMID:8380966  
 A:Accession: S29735  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <PHI>  
 C:Keywords: phosphotransferase

Query Match 24.6%; Score 15; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 HNLG 12  
 DB 2 HVLG 5

## RESULT 15

PT0231  
 IG heavy chain CDR3 region (clone 1-118B) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0231  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0231  
 A:Molecule type: DNA  
 A:Residues: 1-9 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 24.6%; Score 15; DB 2; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 FMHNLG 12  
 DB 1 YTHSG 6

Search completed: September 5, 2004, 09:37:44  
 Job time : 10.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds  
(without alignments)  
96.130 Million cell updates/sec

Title: US-09-730-174A-4

Perfect score: 61

Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	37.7	10	1 PSBF CAPAN	Q03367 capsicum an
2	18	29.5	7	1 LANC_CARUI	P36960 capsicum an
3	18	29.5	10	1 HTF1_ROMMI	P18110 ronalea mic
4	16	26.2	8	1 ALL6_CVDPO	P82157 cydia pomon
5	16	26.2	10	1 HTF2_CARMO	P11385 carausius m
6	15	24.6	5	1 EIO3_LITRU	P82099 litoria rub
7	15	24.6	8	1 FUSS_FUSSO	P81010 fusarium so
8	15	24.6	10	1 RRP1_PHODV	P35946 phocine dis
9	15	24.6	11	1 EFG_GLOPA	P81350 clostridium
10	15	24.6	11	1 NUHW_CANFA	P49820 canis famil
11	15	24.6	11	1 T2F1_PROVU	P31031 proteus vul
12	14	23.0	4	1 FLRN_ANTEL	P58707 anthopleura
13	14	23.0	7	1 ALL7_CVDPO	P82158 cydia pomon
14	14	23.0	7	1 TY51_LITRU	P82065 litoria rub
15	14	23.0	8	1 ALI8_CARMA	P81821 carcinus ma
16	14	23.0	8	1 ALI1_CVDPO	P82152 cydia pomon
17	14	23.0	8	1 HTF1_PERAM	P04548 periplaneta
18	14	23.0	9	1 FAR8_WACRS	P83281 macrobrachi
19	14	23.0	9	1 UF02_MOUSE	P38640 mus musculu
20	14	23.0	10	1 ALI9_CARMA	P81822 carcinus ma
21	14	23.0	10	1 TKNC_RANCA	P22690 rana catesb
22	14	23.0	10	1 TRNK_PIG	P01292 sus scrofa
23	14	23.0	11	1 ASL1_BACSE	P83146 bacteroides
24	14	23.0	12	1 HCY1_CARMA	P83176 carcinus ma
25	14	23.0	12	1 LMT1_LOCMI	P22395 locusta mig
26	14	23.0	12	1 FORD_METTM	P80903 methanobact
27	14	23.0	12	1 RS19_TOBBP	Q56251 tomato big
28	13	21.3	6	1 TRP1_PSEPU	P36414 pseudomonas
29	13	21.3	8	1 HTP_TENMO	P25419 tenebrio mo
30	13	21.3	8	1 LCK4_LEUMA	P21143 leucophaea
31	13	21.3	8	1 LCK6_LEUMA	P15988 leucophaea
32	13	21.3	9	1 CONO_CONGE	P05486 conus geogr
33	13	21.3	9	1 MOSH_CLYJA	P19852 clypeaster

34 13 21.3 9 1 OXVT\_BISFO P42998 eisenia foe  
35 13 21.3 9 1 PPX1\_PERAM P82691 periplaneta  
36 13 21.3 11 1 ASL2\_BACSE P83147 bacteroides  
37 13 21.3 11 1 COR2\_PERAM P11496 periplaneta  
38 13 21.3 11 1 CS15\_BACSU P81095 bacillus su  
39 13 21.3 11 1 PVX1\_PERAM P41837 periplaneta  
40 13 21.3 11 1 Q2OA\_COMTE P80464 comamonas t  
41 13 21.3 12 1 UKA2\_HUMAN P31144 homo sapien  
42 13 21.3 12 1 UR2\_FOLSP P81022 polyodon sp  
43 12 19.7 5 1 RE31\_LITRU P82071 litoria rub  
44 12 19.7 5 1 RE31\_LITRU P82072 litoria rub  
45 12 19.7 8 1 ANG2\_BOTJA Q10582 bothriops ja

#### ALIGNMENTS

RESULT 1  
PSBF CAPAN STANDARD; PRT; 10 AA.  
ID Q03367;  
AC 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)  
DE (Fragment).  
GN PSBF.  
OS Capsicum annuum (Bell pepper).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiales; Solanales; Solanaceae; Capsicum.  
OX NCBI\_TaxID:4072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;  
RA MEDLINE=9309270; PubMed=1463853;  
RA Kuntz W.; Camara B.; Weil J.-H.; Schantz R.;  
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA  
RT editing also occurs in non-photosynthetic chromoplasts.";  
RL Plant Mol. Biol. 20:1185-1188(1992).  
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the  
CC reaction center of photosystem II and possibly is part of the  
CC water-oxidation complex.  
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.  
CC -!- SIMILARITY: Belongs to the psbE / psbF family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: X65570; CAA46539.1; -.  
DR PIR: S28055; S28055.  
DR HAVAP; MF\_00643; -.  
DR InterPro; IPR006216; Cyt\_b559.  
DR PROSITE; PS00537; CYTOCHROME\_B559; PARTIAL.  
DR Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.  
FT NON\_TER 1 1  
FT TRANSMEM <1 5 BY SIMILARITY.  
FT DOMAIN 6 10 LUMENAL (POTENTIAL).  
FT SEQUENCE 10 AA; 1180 MW; 817D0F59D6D6DC5 CRC64;  
SQ

Query Match 37.7%; Score 23; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFM 8

Db 1 SISAMQFI 8

RESULT 2  
 LANC\_CARUI STANDARD; PRT; 7 AA.  
 AC P3660;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lantibiotic carnocin U149 (Fragment).  
 OS Carnobacterium sp. (strain U149).  
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
 OC Carnobacterium.  
 OX NCBI\_TaxID=35782;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92321768; PubMed=1622206;  
 RA Stoffels G., Nissen-Weyer J., Gudmundsdottir A., Sletten K., Holo H.,  
 Nes I.F.;  
 RT "Purification and characterization of a new bacteriocin isolated from  
 a Carnobacterium sp.;"  
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
 CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).  
 CC Active on Gram-positive bacteria.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6

DB 2 SEIQ 5

RESULT 3  
 HTFL\_ROMMI STANDARD; PRT; 10 AA.  
 AC P8110;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE RO I (Hypertrehalosaemic factor).  
 OS Romalea microptera (rubber grasshopper).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Romaleidae; Romalea.  
 OX NCBI\_TaxID=7007;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Corpora cardiaca;  
 RX MEDLINE=89145002; PubMed=3226948;  
 RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
 RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
 the rubber grasshopper, Romalea microptera.";  
 RL Peptides 9:681-688(1988).  
 CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
 elevate the level of trehalose in the hemolymph of insects).  
 CC major carbohydrate in the hemolymph of insects).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the AKH / RPCH family.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD RES 1  
 FT MOD RES 10  
 SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIOFMENLG 12  
 DB 1 QVNFTPNWG 9

## RESULT 4

ALL6\_CYDPO STANDARD; PRT; 8 AA.  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 6.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Dave H., Joensen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MENLIG 12

DB 3 LYNFG 7

## RESULT 5

HTF2\_CARMO STANDARD; PRT; 10 AA.  
 AC F11385;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypertrehalosaemic factor II (HTF-II) (HPTH-II) (Hypertrehalosaemic  
 neuropeptide II).  
 OS Carausius morosus (Indian stick insect), and  
 OS Exatosoma tiaratum (Stick insect).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;  
 OC Heteronemiidae; Carausius.  
 OX NCBI\_TaxID=7022, 7024;  
 RN [1]  
 RP SEQUENCE.  
 RX SPECIES=C. morosus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=87157103; PubMed=3828078;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structure of the hypertrehalosaemic factor II from the  
 corpus cardiacum of the Indian stick insect, Carausius morosus,  
 determined by fast atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).  
 RN [2]  
 RP SEQUENCE.  
 RX SPECIES=E. tiaratum; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
 the corpora cardiaca of the cockroaches Leucophaea maderae,  
 Gromphadorhina portentosa, Blattella germanica and Blatta orientalis

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RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C.merosus; TISSUE=Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiacum."
RL Biochem. Biophys. Res. Commun. 189:1303-1309 (1992).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; JG1416; JG1416.
DR PIR; S09138; S09138.
DR InterPro; IPR02047; AKH.
DR PROSITE; PS0256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 ETQFMHNLG 12
Db 1 QLTFTPNWG 9

RESULT 6
E103 LITRU
ID E103 LITRU STANDARD; PRT; 5 AA.
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP TISSUE=Skin secretion;
RC Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FMH 9
Db 1 FVH 3

RESULT 7
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FUSS_FUSSO
ID FUSS_FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisii) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Varma J., Gangal S.V.;
RL Submitted (JUL-1997) to Swiss-Prot.
CC -!- ALLERGEN: Causes an allergic reaction in human.
KW Allergen.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11
Db 5 HNV 7

RESULT 8
RRPL PHODV
ID RRPL PHODV STANDARD; PRT; 10 AA.
AC P35946;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster/88;
RX MEDLINE=92268877; PubMed=1588321;
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT "Molecular characterization of phocine distemper virus: gene order
RT and sequence of the gene encoding the attachment (H) protein."
RL J. Gen. Virol. 73:1189-1194 (1992).
CC -!- FUNCTION: Probable component of the active polymerase. It may
CC function in mRNA synthesis, capping, methylation and poly(A)
CC synthesis of newly synthesized viral mRNAs, RNA editing of the P
CC gene transcript, and protein kinase activity.
CC -!- CATALYTIC ACTIVITY: Nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D10371; BAA01208.1;
CC Transferase; RNA-directed RNA polymerase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;
```

Query Match 24.6%; Score 15; DB 1; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5  
 ||:|  
 Db 5 SVNQI 9

## RESULT 9

EFQ\_CLOPA STANDARD; PRT; 11 AA.  
 AC P81350;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (CP 5) (Fragment).  
 GN FUSA.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flensburg R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 sequence analysis of proteins from Clostridium pasteurianum W5.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -|- FUNCTION: This protein promotes the GTP-dependent translocation of  
 the nascent protein chain from the A-site to the P-site of the  
 ribosome.  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -|- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPBind.  
 DR PROSITE; PS00301; EFACTOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71FID9C33B17 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 11;  
 Best Local Similarity 25.0%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 IOFMHNLG 12  
 :|:|  
 Db 4 LEKFNQIG 11

## RESULT 10

NUHM\_CANFA STANDARD; PRT; 11 AA.  
 AC P49820;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-OCT-2003 (Rel. 42, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Fragment).  
 GN NDUFB2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).

CC -|- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)  
 FRAGMENT OF THE ENZYME.  
 CC -|- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -|- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -|- COFACTOR: Binds 1 2Fe-2S cluster (potential).  
 CC -|- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
 CC -|- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the  
 mitochondrial inner membrane.  
 CC -|- SIMILARITY: Belongs to the complex I 24 kDa subunit family.  
 DR HSC-2DPAGE; P49820; DOG.  
 DR InterPro; IPR002023; Cmplx1\_24kDa.  
 DR PROSITE; PS01099; COMPLEX1\_24K; PARTIAL.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
 KW Iron-sulfur; Iron; 2Fe-2S.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FMH 9  
 ||:|  
 Db 7 FVH 9

## RESULT 11

T2P1\_PROVU STANDARD; PRT; 11 AA.  
 ID\_T2P1\_PROVU  
 AC P31031; 1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)  
 DE (R.PvuI) (Fragment).  
 GN PVUIR.  
 OS Proteus vulgaris.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Proteus.  
 OX NCBI\_TaxID=585;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13315;  
 RX MEDLINE=93087186; PubMed=1454536;  
 RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;  
 RT "Cloning and characterization of genes for the PvuI restriction and  
 modification system.";  
 RL Nucleic Acids Res. 20:5743-5747(1992).  
 CC -|- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND  
 CLEAVES AFTER T-4  
 CC -|- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
 specific double-stranded fragments with terminal 5'-phosphates.  
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 CC -----  
 CC EMBL; L04163; AAA25660.1; ..  
 DR PIR; S35490; S35490.  
 DR REBASE; 1541; PvuI.  
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 24.6%; Score 15; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1 SVSEI 5																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Sun Sep 5 09:56:55 2004

FT MOD RES 8 8 AMIDATION (POTENTIAL).  
SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;  
Query Match 23.0%; Score 14; DB 1; Length 8;  
Best/Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 8 MHNLG 12  
|::|  
Db 3 MYSFG 7

Search completed: September 5, 2004, 09:35:03  
Job time : 7.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds  
(without alignments)  
137.681 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61  
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTRMBL 25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mmc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	24	39.3	11	13 Q9PS71	Q9PS71 agkistrodon
2	19	31.1	8	6 Q9TT78	Q9TT78 canis famil
3	19	31.1	9	12 Q92766	Q92766 canine dist
4	19	31.1	9	12 Q71066	Q71066 canine dist
5	19	31.1	12	13 P82081	P82081 limnodynast
6	18	29.5	8	3 Q13591	Q13591 saccharomyc
7	18	29.5	10	4 Q15342	Q15342 homo sapien
8	18	29.5	12	8 Q8MES0	Q8MES0 anoda crist
9	18	29.5	12	15 Q85631	Q85631 avian carci
10	17	27.9	11	5 Q23876	Q23876 dictyosteli
11	17	27.9	11	8 Q35374	Q35374 paramecium
12	16	26.2	7	6 Q28742	Q28742 oryctolagus
13	16	26.2	7	13 Q8J720	Q8J720 gallus gall
14	16	26.2	8	3 Q05403	Q05403 saccharomyc
15	16	26.2	8	10 Q40659	Q40659 oryza sativ
16	16	26.2	8	13 P82082	P82082 limnodynast

17	16	26.2	8	13 P82083	P82083 limnodynast
18	16	26.2	9	2 Q44377	Q44377 aeromonas t
19	16	26.2	9	2 Q44468	Q44468 aeromonas v
20	16	26.2	9	2 Q8XU3	Q8XU3 borrelia bu
21	16	26.2	9	2 Q43928	Q43928 aeromonas p
22	16	26.2	9	2 Q44001	Q44001 aeromonas e
23	16	26.2	9	10 Q9FXL0	Q9FXL0 lilium long
24	16	26.2	11	8 Q9GD68	Q9GD68 elaeis guin
25	16	26.2	11	10 P82336	P82336 pisum sativ
26	16	26.2	12	13 P82085	P82085 limnodynast
27	15	24.6	8	4 Q15894	Q15894 homo sapien
28	15	24.6	8	8 Q34909	Q34909 locusta mig
29	15	24.6	8	13 Q90493	Q90493 epealtria
30	15	24.6	9	2 Q43960	Q43960 acrobacter
31	15	24.6	9	4 Q15891	Q15891 homo sapien
32	15	24.6	9	10 Q8S3C6	Q8S3C6 glycine max
33	15	24.6	9	10 Q9FEC0	Q9FEC0 hordeum vul
34	15	24.6	10	5 P82222	P82222 bombyx mori
35	15	24.6	10	10 Q8GZC8	Q8GZC8 hordeum vul
36	15	24.6	10	11 Q61807	Q61807 mus musculu
37	15	24.6	11	3 Q9UR35	Q9UR35 pichia angu
38	15	24.6	11	4 Q9C057	Q9C057 homo sapien
39	15	24.6	11	6 Q9BDC8	Q9BDC8 pongo pygma
40	15	24.6	11	6 Q9BDQ9	Q9BDQ9 gorilla gor
41	15	24.6	11	6 Q9BDD0	Q9BDD0 pan troglod
42	15	24.6	11	6 Q9BDC9	Q9BDC9 pan paniscu
43	15	24.6	12	4 Q9UNV5	Q9UNV5 homo sapien
44	14	23.0	7	8 Q99182	Q99182 gnatholebia
45	14	23.0	8	12 Q91U19	Q91U19 influenza a

## ALIGNMENTS

## RESULT 1

Q9PS71 ID Q9PS71 PRELIMINARY; PRT; 11 AA.  
AC Q9PS71;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Fibrinolytic metalloproteinase (fragment).  
OS Agkistrodon contortrix.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Agkistrodon.  
CX NCBI\_TaxID=8720;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91378546; PubMed=1898066;  
RA Guan A.L., Retzius A.D., Henderson G.N., Markland F.S.Jr.;  
RT "Purification and characterization of a fibrinolytic enzyme from venom  
of the southern copperhead snake (Agkistrodon contortrix  
contortrix)";  
RL Arch. Biochem. Biophys. 289:197-207(1991).  
FT NON-TER 11  
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E872B CRC64;

Query Match 39.3%; Score 24; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12  
|||  
Db 7 HNLG 10

## RESULT 2

Q9TT78 ID Q9TT78 PRELIMINARY; PRT; 8 AA.  
AC Q9TT78;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026234; AAC09164.1;
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 10
Db 1 MHN 3

RESULT 5
P82081 PRELIMINARY; PRT; 12 AA.
ID P82081
AC P82081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DYNASTIN 3.
OS Limnodynastes terraereginae (Northern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=104894;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=TESTIS GLAND;
RA Rattery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT Limnodynastes terraereginae.";
RL Aust. J. Chem. 46:833-842 (1993).
CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAE.
SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

Query Match 31.1%; Score 19; DB 13; Length 12;
Best Local Similarity 60.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 12
Db 7 LNN 11

RESULT 6
O13591 PRELIMINARY; PRT; 8 AA.
ID O13591
AC O13591;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026234; AAC09164.1;
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 10
Db 1 MHN 3

RESULT 5
P82081 PRELIMINARY; PRT; 12 AA.
ID P82081
AC P82081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DYNASTIN 3.
OS Limnodynastes terraereginae (Northern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=104894;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=TESTIS GLAND;
RA Rattery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT Limnodynastes terraereginae.";
RL Aust. J. Chem. 46:833-842 (1993).
CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAE.
SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

Query Match 31.1%; Score 19; DB 13; Length 12;
Best Local Similarity 60.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 12
Db 7 LNN 11

RESULT 6
O13591 PRELIMINARY; PRT; 8 AA.
ID O13591
AC O13591;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026234; AAC09164.1;
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 10
Db 1 MHN 3

RESULT 5
P82081 PRELIMINARY; PRT; 12 AA.
ID P82081
AC P82081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DYNASTIN 3.
OS Limnodynastes terraereginae (Northern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=104894;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=TESTIS GLAND;
RA Rattery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT Limnodynastes terraereginae.";
RL Aust. J. Chem. 46:833-842 (1993).
CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAE.
SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

Query Match 31.1%; Score 19; DB 13; Length 12;
Best Local Similarity 60.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 12
Db 7 LNN 11

RESULT 6
O13591 PRELIMINARY; PRT; 8 AA.
ID O13591
AC O13591;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026237; AAC09167.1;
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 10
Db 1 MHN 3

RESULT 4
O71066 PRELIMINARY; PRT; 9 AA.
ID O71066
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (Fragment).
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026237; AAC09167.1;
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MHN 10
Db 1 MHN 3

RESULT 4
O71066 PRELIMINARY; PRT; 9 AA.
ID O71066
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (Fragment).
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
```

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RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CAA96271.2; -.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E49C9C720 CRC64;

Query Match 29.5%; Score 18; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMHN 10
Db 4 FNHN 7

RESULT 7
Q15342 PRELIMINARY; PRT; 10 AA.
AC Q15342;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Aml1 protein (Fragment).
GN AML1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=96226397; PubMed=8634147;
RA Levanon D., Bernstein Y., Negraru V., Ghozi M.C., Bar-Am I.,
RA Aloya R., Goldenberg D., Lotem J., Groner Y.;
RT "A large variety of alternatively spliced and differentially expressed
RT mRNAs are encoded by the human acute myeloid leukemia gene AML1."
RL DNA Cell Biol. 15:175-185(1996).
DR EMBL; X90978; CAA62455.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1254 MW; 8D99287B441AF365 CRC64;

Query Match 29.5%; Score 18; DB 4; Length 10;
Best Local Similarity 44.4%; Pred. No. 8.8e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 SVSWXRYPH 9

RESULT 8
Q8MES0 PRELIMINARY; PRT; 12 AA.
AC Q8MES0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Anoda cristata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Anoda.
OX NCBI_TaxID=183227;
RN [1]_
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384567; AAM50405.1; -.
GO; GO:0009507; Chloroplast; IEA.

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KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1431 MW; 9A5E59B65452C9CA CRC64;

Query Match 29.5%; Score 18; DB 8; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 BQFMHNL 11
Db 3 EPDFVNNI 10

RESULT 9
Q85631 PRELIMINARY; PRT; 12 AA.
AC Q85631;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MH2, proviral DNA, myc to 3' LTR (Fragment).
OS Avian carcinoma virus.
OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11958;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=85033920; PubMed=6092695;
RA Surave P., Jansen H.W., Bister K., Rapp U.R.;
RT "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT elements with avian sarcoma viruses Y73 and SR-A."
RL J. Virol. 52:703-705(1984).
DR EMBL; K03100; AAA42388.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1466 MW; 72E4B884F30736DB CRC64;

Query Match 29.5%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11
Db 2 HNL 4

RESULT 10
Q23876 PRELIMINARY; PRT; 11 AA.
AC Q23876;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 09, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=82260445; PubMed=6286214;
RA McKeown M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL; K02957; AAA33150.1; -.
DR EMBL; K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match 27.9%; Score 17; DB 5; Length 11;
Best Local Similarity 28.6%; Pred. No. 1.5e+04;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 BQFMHNL 10
Db 5 DVQALNN 11

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RESULT 11
Q35374 PRELIMINARY; PRT; 11 AA.
ID Q35374
AC Q35374;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE P1 protein (Fragment).
OS Parametium tetraurelia.
OG Mitochondrion.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Parametium.
OC NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=stock 172; PubMed=3023187;
RX MEDLINE=87055241;
RA Pritchard A.E., Seilhamer J.J., Cummings D.J.;
RT "Parametium mitochondrial DNA sequences and RNA transcripts for
RT cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the
RT replication origin.";
RL Gene 44:243-253(1986).
DR EMBL; M15280; AAA79267.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

Query Match 27.9%; Score 17; DB 8; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6
Db 2 SLNQIQ 7

RESULT 12
Q28742 PRELIMINARY; PRT; 7 AA.
ID Q28742
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
DR PIR; I46868;
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 26.2%; Score 16; DB 6; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMHN 10
Db 1 QKXHD 5

RESULT 13
Q8JU20 PRELIMINARY; PRT; 7 AA.
ID Q8JU20
AC Q8JU20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Extracellular fatty acid binding protein (Fragment).
GN EXPABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of 3' UTR of EXPABP gene in chicken.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF487519; AAL96665.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEI 5
Db 3 SVDEV 7

RESULT 14
Q05403 PRELIMINARY; PRT; 8 AA.
ID Q05403
AC Q05403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE DNA for ORF's from chromosome XV (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zundstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 26.2%; Score 16; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHNL 11
Db 2 IHNV 5

RESULT 15
Q40659 PRELIMINARY; PRT; 8 AA.
ID Q40659
AC Q40659;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078641; PubMed=2258052;
RA Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomycers
RT cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
DR Gramene; Q40659; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 26.2%; Score 16; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. NO. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 IOFMHNL 11
Db 1 MQVLNNW 7

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Search completed: September 5, 2004, 09:37:00  
 Job time : 28.5 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds  
(without alignments)  
92.892 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61  
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1980s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	82.0	11	6	ABG72607 Parathyro
2	50	82.0	12	6	ABG72608 Parathyro
3	46	75.4	11	3	AAY96968 Parathyro
4	45	73.8	10	2	AAR91644 Human par
5	45	73.8	10	3	AAY68767 Amino aci
6	45	73.8	10	4	AAB86219 Human par
7	45	73.8	10	6	ABR44166 Human par
8	41	67.2	9	4	AAB86225 Human par
9	39	63.9	9	2	AAR91645 Human par
10	39	63.9	9	3	AAY96981 Parathyro
11	39	63.9	9	4	AAB86220 Human par
12	38.5	63.1	11	2	AAY50600 Resin bou
13	36	59.0	9	3	AAB01862 PTH(1-14)
14	36	59.0	9	3	AAY96966 Parathyro
15	33	54.1	9	3	AAB01863 PTH(1-14)
16	33	54.1	10	4	AAB96932 Rat parat
17	33	54.1	11	4	AAB96931 Rat parat
18	33	54.1	11	4	AAB96915 Parathyro
19	33	54.1	11	4	AAB84770 Parathyro
20	33	54.1	12	4	AAB96914 Parathyro
21	33	54.1	12	4	AAB84769 Parathyro
22	32	52.5	9	3	AAY78849 Parathyro
23	31	50.8	8	2	AAR91646 Human par
24	31	50.8	8	3	AAB07467 Antigenic
25	31	50.8	8	4	AAB86221 Human par

26	31	50.8	10	6	ABP71484
27	31	50.8	11	6	ABP71485
28	31	50.8	11	6	ABP71483
29	31	50.8	12	2	AAM45785
30	31	50.8	12	6	ABP71482
31	29	47.5	9	3	AAB01866
32	28	45.9	11	1	AAP82547
33	28	45.9	11	4	AAB96892
34	28	45.9	12	4	AAB96891
35	27	44.3	10	5	ABG9386
36	27	44.3	11	4	ABU94029
37	26	42.6	6	2	AAR91648
38	26	42.6	6	3	AAY68764
39	26	42.6	6	4	AAB86223
40	26	42.6	6	6	ABR44168
41	26	42.6	7	2	AAR91647
42	26	42.6	7	3	AAB00068
43	26	42.6	7	4	AAB86222
44	26	42.6	9	3	AAB01864
45	26	42.6	9	3	AAY97062

#### ALIGNMENTS

RESULT 1  
ABG72607  
ID ABG72607 standard; peptide; 11 AA.

AC ABG72607;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Parathyroid hormone antigenic peptide 2-12.  
XX

KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX Homo sapiens.  
OS Mus sp.  
OS Rattus sp.  
OS Bos taurus.  
OS Sus scrofa.  
OS Canis familiaris.

XX Key Location/Qualifiers  
FH Misc-difference 6  
FT /label= Leu, Phe

XX US2002110871-A1.  
XX 15-AUG-2002.

XX 05-DEC-2000; 2000US-00730174.

XX 05-DEC-2000; 2000US-00730174.

XX (ZAHN/) ZAHRADNIK R J.  
XX (LAVI/) LAVIGNE J R.

XX Zahradnik RJ, Lavigne JR;

XX WPI; 2003-066685/06.

XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
and isolation of antibodies having an affinity to it, useful for  
determining bioactive PTH levels in serum, plasma and/or cell culture  
media.

XX Claim 1; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
formation and isolation of antibodies having an affinity to it, being

CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are; (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH  
 XX  
 SQ Sequence 11 AA;

Query Match 82.0%; Score 50; DB 6; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.01;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIQFMHNLG 12  
 DB 1 VSEIQFMHNLG 11  
 ||||| |||||  
 ||||| |||||

RESULT 2  
 ABG72608  
 ID ABG72608 standard; peptide; 12 AA.

AC ABG72608;  
 XX  
 DT 11-FEB-2003 (first entry)  
 XX  
 DE Parathyroid hormone antigenic peptide 1-12.  
 XX  
 KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
 KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX Homo sapiens.  
 OS Mus sp.  
 OS Rattus sp.  
 OS Bos taurus.  
 OS Sus scrofa.  
 OS Canis familiaris.

XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /label= Ser, Ala  
 FT FT  
 FT Misc-difference 7 /label= Leu, Phe  
 FT FT

XX US2002110871-A1.  
 XX  
 XX 15-AUG-2002.  
 XX  
 XX 05-DEC-2000; 2000US-00730174.  
 XX  
 XX 05-DEC-2000; 2000US-00730174.

XX (ZHR/) ZHRADNIK R J.  
 XX (LAVI/) LAVIGNE J R.  
 XX Zahradnik RJ, Lavigne JR;  
 PI

XX WPI; 2003-066695/06.  
 XX  
 XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
 XX and isolation of antibodies having an affinity to it, useful for  
 XX determining bioactive PTH levels in serum, plasma and/or cell culture  
 XX media.  
 XX  
 XX Claim 2; Page 5; 11pp; English.  
 XX  
 XX The invention relates to a new antigenic peptide for inducing the  
 XX formation and isolation of antibodies having an affinity to it, being  
 XX formed from the N-terminus of parathyroid hormone (PTH). Also included  
 XX are; (1) a method for producing antibodies useful in the determination of  
 XX PTH levels in a biological sample comprising: (a) providing at least one  
 XX first peptide antigen comprising a peptide fragment of PTH; (b)  
 XX administering the first peptide antigen to a host animal to induce  
 XX antibody production; (c) monitoring the antibody titre produced; (d)  
 XX isolating antisera produced in the host animal; and (e) selecting  
 XX antisera from the isolated antisera produced in the host that is capable  
 XX of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 XX the method; and (3) test kits and analytical procedures used for the  
 XX determination of bioactive intact PTH utilising (ab). The methods and  
 XX compositions of the present invention are useful for determining  
 XX bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 XX The antigens, antibodies and methods of the present invention, as  
 XX compared to prior art, have the particular advantages of possessing  
 XX greater affinity for PTH, and in particular, are designed to have a novel  
 XX recognition for amino acid residues extending beyond the first N-terminal  
 XX PTH residue, and further have negligible cross-reactivity with the large  
 XX non-molecular forms of PTH. PTH levels are an important parameter in  
 XX patients suffering from hypercalcaemia, osteoporosis and primary  
 XX hyperparathyroidism. The present sequence represents a PTH antigenic  
 XX peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
 XX canine and bovine PTH  
 XX  
 SQ Sequence 12 AA;

Query Match 82.0%; Score 50; DB 6; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.01;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMHNLG 12  
 DB 2 VSEIQFMHNLG 12  
 ||||| |||||  
 ||||| |||||

RESULT 3  
 AAY96968  
 ID AAY96968 standard; peptide; 11 AA.

XX  
 AC AAY96968;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX

XX Parathyroid hormone N-terminal signaling domain (residues 1-11).  
 XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 XX bone reformation; resorption; remodeling; tether1; osteoporosis.

XX Homo sapiens.  
 XX  
 XX WO200039278-A2.  
 XX  
 XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.  
 XX  
 XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 PA

PA (JUEP/) JUEPPNER H.  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-452384/39.  
 XX  
 XX New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 PT  
 XX Claim 4; Page 92; 119pp; English.  
 XX  
 XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n  
 CC -R, are new. S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R1 is the  
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased tether activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 75.4%; Score 46; DB 3; Length 11;  
 Best Local Similarity 81.8%; Pred. No. 0.059;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNL 11  
 :|||||  
 Db 1 AVSEIQLMNL 11

RESULT 4  
 AAR91644  
 ID AAR91644 standard; peptide; 10 AA.  
 XX  
 AC AAR91644;  
 XX  
 DT 06-NOV-1996 (first entry)  
 XX  
 XX Human parathyroid hormone antigenic peptide hPTH 1-10.  
 DE  
 XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 KW  
 XW diagnosis; active hPTH 1-37.  
 XX  
 XX Synthetic.  
 OS  
 XX DE4434551-A1.  
 PN  
 XX 04-APR-1996.  
 PD  
 XX 28-SEP-1994; 94DE-04434551.  
 PF  
 XX 28-SEP-1994; 94DE-04434551.  
 PR  
 XX (FORS/) FORSSMANN W.  
 PA  
 XX Adermann K, Forssmann W, Hock D, Maegerlein M;  
 PI  
 XX WPI; 1996-180391/19.  
 DR  
 XX New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 PT generated using them, able to distinguish between active and inactive  
 PT forms of the hormone.  
 XX  
 PS Claim 2; Page 4; 5pp; German.  
 XX

CC The present sequence is a specific example of claimed immunogenic  
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 CC terminal alpha-helical region and/or the non-structured region of the  
 CC hormone. Antibodies and their binding fragments generated by injecting an  
 CC animal with the peptides are useful as diagnostic reagents for  
 CC determination of biologically active hPTH(1-37)  
 XX  
 XX Sequence 10 AA;  
 SQ

Query Match 73.8%; Score 45; DB 2; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.082;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHN 10  
 :|||||  
 Db 1 SVSEIQLMHN 10

RESULT 5  
 AAY68767  
 ID AAY68767 standard; peptide; 10 AA.  
 XX  
 AC AAY68767;  
 XX  
 DT 05-MAY-2000 (first entry)  
 XX  
 XX Amino acids 1-10 of a parathyroid hormone (PTH).  
 DE  
 XX Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
 KW slimming treatment; cellulite; skin firming.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200004047-A1.  
 PN  
 XX 27-JAN-2000.  
 PD  
 XX 07-JUL-1999; 99WO-FR001687.  
 DF  
 XX 17-JUL-1998; 98FR-00009193.  
 PR  
 XX (SEDE-) SEDERMA.  
 PA  
 XX Lintner K;  
 PI  
 XX WPI; 2000-171243/15.  
 DR  
 XX New parathyroid hormone fragment peptides, used as lipolysis stimulants  
 PT in topically applied cosmetic compositions for slimming treatment of  
 PT excessive weight in hips and thighs.  
 XX  
 XX Claim 1; Page 8; 18pp; French.  
 PS  
 XX The present sequence represents a parathyroid hormone (PTH) fragment,  
 CC comprising amino acids 1-10. Parathyroid hormone fragments of the  
 CC invention have lipolysis stimulating activity (especially when topically  
 CC administered). The lipolytic activity of the peptides is enhanced when  
 CC they are chemically modified to increase their lipophilicity. The  
 CC peptides are used in cosmetic or dermatological compositions for skin  
 CC care. They are especially used for slimming treatment of excessive weight  
 CC in the thighs and hips, in the treatment of cellulite and for skin  
 CC firming  
 XX  
 XX Sequence 10 AA;  
 SQ

Query Match 73.8%; Score 45; DB 3; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.082;  
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHN 10  
 :|||||  
 Db 1 SVSEIQLMHN 10

RESULT 6  
AAB86219  
ID AAB86219 standard; peptide; 10 AA.  
AC AAB86219;  
XX  
XX 03-SEP-2001 (first entry)  
XX  
XX Human parathyroid hormone immunogenic peptide SEQ ID 1.  
DE  
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KW hypo-parathyroidism; hyper-parathyroidism.  
XX  
XX Homo sapiens.  
OS  
XX DE19961350-A1.  
PN  
XX 21-JUN-2001.  
PD  
XX 17-DEC-1999; 99DE-01061350.  
PF  
XX 17-DEC-1999; 99DE-01061350.  
PR  
XX (IMMU-) IMMUNDIAGNOSTIK AG.  
PA  
XX Armbruster FP;  
PI  
XX WPI; 2001-376318/40.  
DR  
XX  
XX Determining the content of physiologically active parathyroid hormone,  
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
PT reactive with different epitopes.  
XX  
XX Disclosure; Page 3; 10pp; German.  
PS  
XX This invention describes a novel method for determining (M1) the content  
CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
CC and including the N-terminal residue and (ii) antibody (Ab2) that  
CC recognizes an epitope within the receptor-binding site of (A). The number  
CC of molecules that react with both antibodies is determined and used to  
CC calculate the content of physiologically active (A). The method is used  
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
CC active and (ii) that apparently intact peptide may be biologically  
CC inactive, and also takes into account the fact that some fragments of (A)  
CC are antagonistic (these have the receptor-binding site but lack the N-  
CC terminus). It thus provides a true measure of the content of  
CC physiologically active (A); contrast methods that measure intact peptide  
CC and its 1-37 fragment which may produce falsely high values. This  
CC sequence represents a peptide fragment used to illustrate the method of  
CC the invention  
XX  
XX Sequence 10 AA;  
SQ

Query Match 73.8%; Score 45; DB 4; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.082;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SVSEIQFMHN 10  
DB 1 SVSEIQFMHN 10  
||| |||  
RESULT 7  
ABR44166  
ID ABR44166 standard; peptide; 10 AA.  
XX  
XX ABR44166;  
AC  
XX

04-AUG-2003 (first entry)  
XX Human parathyroid hormone (hPTH) fragment (residues 1-10).  
XX Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;  
KW lipolysis; human; hPTH.  
XX  
XX Homo sapiens.  
OS  
XX WO2003035697-A1.  
PN  
XX 01-MAY-2003.  
PD  
XX 06-MAY-2002; 2002WO-KR000835.  
PF  
XX 27-SEP-2001; 2001KR-00060245.  
PR  
XX 15-MAR-2002; 2002KR-00014062.  
PR  
XX (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.  
PA  
XX Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;  
PI Chang W;  
PI  
XX WPI; 2003-468288/44.  
DR  
XX Novel fusion peptide comprising self cell-penetrating Tat peptide bound  
PT to human parathyroid hormone-derived peptide, useful as component of skin  
PT slimming cosmetic composition.  
XX  
XX Claim 5; Page 6; 32pp; English.  
PS  
XX The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-  
CC penetrating Tat peptide is bound to human parathyroid hormone-derived  
CC peptide (hPTHDP). The fusion peptide is useful as a component of skin  
CC slimming cosmetic composition. The fusion peptide does not cause  
CC irritation, easily and safely penetrates into integument and endothelium,  
CC does not cause skin disease and has superior lipolysis effects, and is  
CC durable. The present sequence represents a human parathyroid hormone  
CC (hPTH) fragment that can be used to construct the fusion peptide  
XX  
XX Sequence 10 AA;  
SQ

Query Match 73.8%; Score 45; DB 6; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.082;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SVSEIQFMHN 10  
DB 1 SVSEIQFMHN 10  
||| |||  
RESULT 8  
AAB86225  
ID AAB86225 standard; peptide; 9 AA.  
XX  
XX AAB86225;  
AC  
XX  
XX 03-SEP-2001 (first entry)  
DT  
XX Human parathyroid hormone immunogenic peptide SEQ ID 7.  
DE  
XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
KW hypo-parathyroidism; hyper-parathyroidism.  
XX  
XX Homo sapiens.  
OS  
XX DE19961350-A1.  
PN  
XX 21-JUN-2001.  
PD  
XX 17-DEC-1999; 99DE-01061350.  
PF  
XX  
XX



CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis

XX Sequence 9 AA;  
 SQ

Query Match 63.9%; Score 39; DB 3; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
 |||||  
 DB 1 SVSEIQLMH 9

RESULT 11  
 AAB86220  
 ID AAB86220 standard; peptide; 9 AA.

XX AAB86220;

XX 03-SEP-2001 (first entry)

DE Human parathyroid hormone immunogenic peptide SEQ ID 2.

XX Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.

XX Homo sapiens.

XX DE19961350-A1.

XX 21-JUN-2001.

XX 17-DEC-1999; 99DE-01061350.

XX 17-DEC-1999; 99DE-01061350.

XX (IMU-) IMMUNDIAGNOSTIK AG.

XX Armbruster FP;

XX WPI; 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,  
 XX useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 XX reactive with different epitopes.

XX Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention

XX Sequence 9 AA;

Query Match 63.9%; Score 39; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9  
 |||||  
 DB 1 SVSEIQLMH 9

RESULT 12  
 AAY50600

ID AAY50600 standard; peptide; 11 AA.

XX AAY50600;

XX 09-FEB-2000 (first entry)

XX Resin bound cyclic peptide 33.

XX Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
 KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;  
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "FMOC-Ala"

FT Misc-difference 3 /note= "Ser(OtBu)"

FT Misc-difference 4 /note= "Glu(OtBu)"

FT Misc-difference 6 /note= "Gln(Trt)"

FT Misc-difference 9 /note= "His(Trt)"

FT Misc-difference 10 /note= "Asn(Trt)"

XX WO9952933-A1.

XX 21-OCT-1999.

XX 15-APR-1999; 99WO-US008435.

XX 15-APR-1998; 98US-0081897P.

XX (RHON) RHONE-POULENC RORER PHARM INC.

XX Siedeski AW, Mancel JJ;

XX WPI; 1999-633822/54.

XX Convergent synthesis of peptides for treating e.g. bone disorders.

XX Disclosure; Page 75; 85pp; English.

XX This invention describes a novel method for the preparation of peptides  
 CC (ii) that contain both cyclic and linear peptide fragments comprises  
 CC sequential reaction of a resin-bound linear fragment with the cyclic  
 CC fragment in N-protected form and optionally other linear fragments. The  
 CC products of the invention have osteopathic and hypotensive activity. (ii)  
 CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The  
 CC method is particularly used to prepare cyclic peptide analogs of  
 CC parathyroid hormone (PTH) or PTH-related peptides which are useful for  
 CC treating diseases that respond to treatment with agents that bind to PTH  
 CC receptors (with or without activation of adenylyl cyclase activity), e.g.  
 CC hyper- or hypo-calcaemia, osteoporosis, osteopenia, hyper- or hypo-  
 CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also  
 CC for promoting repair of bone fractures. Separate synthesis of the cyclic  
 CC fragment allows convergent synthesis of resin-bound (ii), with better  
 CC yields and higher throughput. The difficulties associated with  
 CC preparation of the bridged fragment are confined to a small peptide which

CC can be purified before reaction with the resin-bound component. AAY50568-  
 CC Y50614 represent the peptide fragments described in the method of the  
 CC invention  
 CC  
 XX Sequence 11 AA;  
 SQ

Query Match 63.1%; Score 38.5; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.5;  
 Matches 9; Conservative 2; Mismatches 0; Indels 1; Gaps 1;  
 XX

Qy 1 SVSEIQFMNLG 12  
 :|||||  
 Db 1 AVSEIQ-LHNLG 11

RESULT 13  
 AAB01862  
 ID AAB01862 standard; peptide; 9 AA.  
 XX  
 AC AAB01862;  
 XX

DT 11-SEP-2000 (first entry)  
 XX

DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.  
 XX

XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200023594-A1.  
 XX  
 XX 27-APR-2000.  
 PD  
 XX  
 XX 20-OCT-1999; 99WO-US024481.  
 PF  
 XX  
 XX 22-OCT-1998; 98US-0105530P.  
 PR  
 XX  
 XX (GARD/) GARDELLA T J.  
 PA (KRON/) KRONENBERG H M.  
 PA (POTT/) POTTS J T.  
 PA (JUEP/) JUEPPNER H.  
 XX

GI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX  
 XX WPI; 2000-339693/29.  
 DR  
 XX  
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 PT acids that encode them, useful for treating osteoporosis.  
 XX  
 XX Disclosure; Page 26; 73pp; English.  
 PS

CC The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance, and vitamin D synthesis in the kidney. A homologous  
 CC callus of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1

CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterized by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodeling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists

XX Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9  
 :|||||  
 Db 1 AVSEIQLMH 9

RESULT 14

AAAY96966  
 ID AAY96966 standard; peptide; 9 AA.  
 XX  
 AC AAY96966;  
 XX

DT 31-OCT-2000 (first entry)  
 XX

DE Parathyroid hormone N-terminal signaling domain (residues 1-9).

XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
 XX

OS Homo sapiens.

XX WO200039278-A2.  
 EN

XX 06-JUL-2000.  
 PD

XX 30-DEC-1999; 99WO-US031108.  
 PF

XX 31-DEC-1998; 98US-0114577P.  
 PR

XX (GARD/) GARDELLA T J.  
 PA (KRON/) KRONENBERG H M.  
 PA (POTT/) POTTS J T.  
 PA (JUEP/) JUEPPNER H.  
 XX

PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.  
 DR

XX New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 XX

PS Claim 4; Page 92; 119pp; English.

XX Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n  
 CC -R, are new. S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether1 activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9  
 :|||||  
 Db 1 AVSEIQLMH 9

## RESULT 15

AAB01863  
 ID AAB01863 standard; peptide; 9 AA.

XX AC AAB01863;

DT 11-SEP-2000 (first entry)

XX PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.

XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.

XX Homo sapiens.  
 CS Synthetic.

XX WO200023594-A1.

XX 27-APR-2000.

XX 20-OCT-1999; 99WO-US024481.

XX 22-OCT-1998; 98US-0105530P.

XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (BOTT/) POTTS J T.  
 XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-339693/29.

XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 PT acids that encode them, useful for treating osteoporosis.

XX Disclosure; Page 26; 73pp; English.

XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Ileu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous

CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterised by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodelling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists  
 XX  
 SQ Sequence 9 AA;

Query Match 54.1%; Score 33; DB 3; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SVSEIQFMH 9  
 :|||||  
 Db 1 AVSEIQLMH 9

Search completed: September 5, 2004, 09:34:30  
 Job time : 36.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds  
(without alignments)  
116.332 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61  
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	12	9 US-09-730-174A-4	Sequence 4, Appli
2	58	95.1	12	9 US-09-730-174A-6	Sequence 6, Appli
3	57	93.4	11	9 US-09-730-174A-2	Sequence 2, Appli
4	55	90.2	12	9 US-09-730-174A-3	Sequence 3, Appli
5	52	85.2	12	9 US-09-730-174A-5	Sequence 5, Appli
6	51	83.6	11	9 US-09-730-174A-1	Sequence 1, Appli
7	45	73.8	10	14 US-10-168-185-1	Sequence 1, Appli
8	41	67.2	9	14 US-10-168-185-7	Sequence 7, Appli
9	39	63.9	9	14 US-10-168-185-2	Sequence 2, Appli
10	37	60.7	8	14 US-10-168-185-8	Sequence 8, Appli
11	36	59.0	9	14 US-10-192-673-6	Sequence 6, Appli
12	33	54.1	9	14 US-10-192-673-7	Sequence 7, Appli
13	31	50.8	8	14 US-10-168-185-3	Sequence 3, Appli
14	29	47.5	9	14 US-10-192-673-10	Sequence 10, Appli
15	27	44.3	10	14 US-10-033-741-61	Sequence 61, Appli

16	26	42.6	6	14	US-10-168-185-5	Sequence 5, Appli
17	26	42.6	7	14	US-10-168-185-4	Sequence 4, Appli
18	26	42.6	9	14	US-10-192-673-8	Sequence 8, Appli
19	26	42.6	10	14	US-10-168-185-11	Sequence 11, Appli
20	25	41.0	10	15	US-10-137-867-526	Sequence 526, App
21	25	41.0	10	15	US-10-366-709-2	Sequence 2, Appli
22	24	39.3	9	9	US-09-834-765-45	Sequence 45, Appli
23	24	39.3	9	9	US-09-834-765-55	Sequence 55, Appli
24	24	39.3	9	9	US-09-746-945-6	Sequence 6, Appli
25	24	39.3	10	9	US-09-834-765-73	Sequence 73, Appli
26	24	39.3	10	9	US-09-834-765-78	Sequence 78, Appli
27	24	39.3	10	14	US-10-232-187-8	Sequence 8, Appli
28	24	39.3	11	14	US-10-153-334-14	Sequence 14, Appli
29	24	39.3	11	16	US-10-391-364-93	Sequence 93, Appli
30	24	39.3	12	14	US-10-319-130-16	Sequence 16, Appli
31	23	37.7	8	14	US-10-043-487-508	Sequence 508, App
32	23	37.7	9	14	US-10-147-140-26	Sequence 26, Appli
33	23	37.7	9	15	US-10-024-652-120	Sequence 120, App
34	23	37.7	9	15	US-10-024-652-339	Sequence 339, App
35	23	37.7	9	15	US-10-024-652-407	Sequence 407, App
36	23	37.7	9	15	US-10-024-652-956	Sequence 956, App
37	23	37.7	9	15	US-10-024-652-1094	Sequence 1094, App
38	23	37.7	9	15	US-10-024-652-1259	Sequence 1259, App
39	23	37.7	9	15	US-10-024-652-1385	Sequence 1385, App
40	23	37.7	9	15	US-10-024-652-1464	Sequence 1464, App
41	23	37.7	9	15	US-10-024-652-2057	Sequence 2057, App
42	23	37.7	9	15	US-10-024-652-2058	Sequence 2058, App
43	23	37.7	10	9	US-09-976-787-4	Sequence 4, Appli
44	23	37.7	10	9	US-09-865-198-4	Sequence 4, Appli
45	23	37.7	10	9	US-09-965-099-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1  
US-09-730-174A-4  
; Sequence 4, Application US/09730174A  
; Patent No. US20020110871A1  
; GENERAL INFORMATION:  
; APPLICANT: Zahradnik, R.J.  
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having  
; FILE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H  
; FILE REFERENCE: IMUNE-001A  
; CURRENT APPLICATION NUMBER: US/09/730,174A  
; CURRENT FILING DATE: 2000-12-05  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-4

Query Match 100.0%; Score 61; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNLG 12  
| | | | | | | | | | | |  
Db 1 SVSEIQFMHNLG 12

RESULT 2  
US-09-730-174A-6  
; Sequence 6, Application US/09730174A  
; Patent No. US20020110871A1  
; GENERAL INFORMATION:  
; APPLICANT: Zahradnik, R.J.  
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having  
; FILE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H  
; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A  
; CURRENT FILING DATE: 2000-12-05  
; NUMBER OF SEQ ID NOS: 12

QY 1 SVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 12

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-6

Query Match 95.1%; Score 58; DB 9; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.00054;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 12

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

## RESULT 3

US-09-730-174A-2

; Sequence 2, Application US/09730174A

; Patent No. US20020110871A1

; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.

; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho

; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A

; CURRENT FILING DATE: 2000-12-05

; NUMBER OF SEQ ID NOS: 12

QY 1 SVSEIQFMHNLG 12

Db 1 AVSEIQFMHNLG 12

LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-2

Query Match 93.4%; Score 57; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00075;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 11

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

## RESULT 4

US-09-730-174A-3

; Sequence 3, Application US/09730174A

; Patent No. US20020110871A1

; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.

; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho

; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A

; CURRENT FILING DATE: 2000-12-05

; NUMBER OF SEQ ID NOS: 12

QY 2 SVSEIQFMHNLG 12

Db 1 AVSEIQFMHNLG 11

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-3

Query Match 90.2%; Score 55; DB 9; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0019;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNLG 12  
Db 1 SVSEIQFMHNLG 12

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

## RESULT 5

US-09-730-174A-5

; Sequence 5, Application US/09730174A

; Patent No. US20020110871A1

; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.

; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho

; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A

; CURRENT FILING DATE: 2000-12-05

; NUMBER OF SEQ ID NOS: 12

QY 1 SVSEIQFMHNLG 12

Db 1 AVSEIQFMHNLG 12

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-5

Query Match 85.2%; Score 52; DB 9; Length 12;  
Best Local Similarity 83.3%; Pred. No. 0.0089;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 12

LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence

## RESULT 6

US-09-730-174A-1

; Sequence 1, Application US/09730174A

; Patent No. US20020110871A1

; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.

; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho

; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A

; CURRENT FILING DATE: 2000-12-05

; NUMBER OF SEQ ID NOS: 12

QY 1 SVSEIQFMHNLG 12

Db 1 AVSEIQFMHNLG 11

LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-1

Query Match 83.8%; Score 51; DB 9; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 11

LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

## RESULT 7

US-10-168-185-1

; Sequence 1, Application US/10168185

; Publication No. US20030175802A1

; GENERAL INFORMATION:

; APPLICANT: Ambruster, Franz Paul

; APPLICANT: Missbichler, Albert

; APPLICANT: Schmidt-Gayk, Heinrich

; APPLICANT: Roth, Heinz-Jurgen

; TITLE OF INVENTION: Method for Determining Parathormone

```
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-1

Query Match      73.8%; Score 45; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 SVSEIQFMHN 10
DB      1 SVSEIQLMHN 10

RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match      67.2%; Score 41; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      2 VSEIQFMHN 10
DB      1 VSEIQLMHN 9

RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-2

Query Match      63.9%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 SVSEIQFMHN 9
DB      1 SVSEIQLMHN 9

RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-8

Query Match      60.7%; Score 37; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      3 SEIQFMHN 10
DB      1 SEIQLMHN 8

RESULT 11
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030186838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
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us-09-730-174a-4.closed.rapp

Sun Sep 5 09:56:55 2004

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; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-6

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Query Match          59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SVSEIQFMH 9
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Db 1 AVSEIQLMH 9

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RESULT 12
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-7

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Query Match          54.1%; Score 33; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 SVSEIQFMH 9
   :|||||
Db 1 AVSEIQLMH 9

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RESULT 13
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample

```

```

; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-3

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Query Match          50.8%; Score 31; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SVSEIQFM 8
   :|||||
Db 1 SVSEIQLM 8

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RESULT 14
US-10-192-673-10
; Sequence 10, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-10

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Query Match          47.5%; Score 29; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 SVSEIQFMH 9
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Db 1 SVSEHQLLH 9

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RESULT 15
US-10-033-741-61
; Sequence 61, Application US/10033741
; Publication No. US20030049640A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Vasc
; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-079
; CURRENT APPLICATION NUMBER: US/10/033,741

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; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 61  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-033-741-61

Query Match 44.3%; Score 27; DB 14; Length 10;  
Best local Similarity 55.6%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SYSEIQFMH 9  
|||: :|  
Db 1 SYSELPVH 9

Search completed: September 5, 2004, 09:49:38  
Job time : 33.5 secs

This Page Blank (uspto)

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:32:03 ; Search time 11 seconds  
(without alignments)  
56.319 Million cell updates/sec

Title: US-09-730-174A-4  
Perfect score: 61 SVSEIQFMHNLG 12  
Sequence: 1

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	75.4	12	4	US-09-442-989-31
2	45	73.8	10	3	US-08-817-547A-1
3	39	63.9	9	3	US-08-817-547A-2
4	36	59.0	9	4	US-09-421-379-6
5	33	54.1	9	4	US-09-421-379-7
6	31	50.8	8	3	US-08-817-547A-3
7	29	47.5	9	4	US-09-421-379-10
8	29	47.5	12	2	US-08-140-137A-12
9	28	45.9	11	6	5460978-3
10	26	42.6	6	3	US-08-817-547A-5
11	26	42.6	7	3	US-08-817-547A-4
12	26	42.6	9	4	US-09-421-379-8
13	25	41.0	12	2	US-08-482-228-42
14	25	41.0	12	3	US-08-482-528-42
15	24	39.3	5	2	US-08-177-109A-56
16	24	39.3	5	2	US-08-687-706-56
17	24	39.3	5	3	US-08-817-547A-17
18	24	39.3	6	3	US-08-817-547A-16
19	24	39.3	7	3	US-08-817-547A-15
20	24	39.3	8	2	US-08-748-021-64
21	24	39.3	8	3	US-08-817-547A-14
22	24	39.3	8	3	US-08-974-297-64
23	24	39.3	9	3	US-08-817-547A-13
24	24	39.3	10	3	US-08-817-547A-7
25	23	37.7	9	1	US-07-822-043-26
26	23	37.7	9	1	US-08-346-485B-26
27	23	37.7	9	3	US-08-977-221-26

Sequence 26, Appl  
Sequence 26, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 97, Appl  
Sequence 12, Appl  
Sequence 49, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 108, App  
Sequence 49, Appl  
Sequence 3, Appl  
Sequence 61, Appl  
Sequence 1, Appl  
Sequence 60, Appl  
Sequence 83, Appl  
Sequence 2, Appl  
Sequence 14, Appl

US-09-483-831B-26  
PCT-US95-06613-26  
US-08-116-778E-9  
US-08-438-562-9  
US-08-483-528B-97  
US-08-783-853A-12  
US-08-836-561-49  
US-09-280-028-12  
US-09-344-050-12  
US-09-393-385B-108  
US-09-434-122-49  
US-09-091-071-3  
US-09-556-605-61  
US-09-064-750-1  
US-09-556-605-60  
US-08-615-181-83  
US-08-555-579-2  
US-08-428-257A-14

## ALIGNMENTS

RESULT 1

US-09-442-989-31  
; Sequence 31, Application US/09442989  
; Patent No. 6569993  
; GENERAL INFORMATION:  
; APPLICANT: Sledeski, Adam W.  
; APPLICANT: Mancel, James J.  
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: A3113B-US  
; CURRENT APPLICATION NUMBER: US/09/442,989  
; CURRENT FILING DATE: 1999-11-18  
; EARLIER APPLICATION NUMBER: 60/081,897  
; EARLIER FILING DATE: 1998-04-15  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)  
; OTHER INFORMATION: FMOC-Ala  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (3)  
; OTHER INFORMATION: Ser (OtBu)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (4)  
; OTHER INFORMATION: Glu (OtBu)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (6)  
; OTHER INFORMATION: Gln (Trt)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (9)  
; OTHER INFORMATION: His (Trt)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (10)  
; OTHER INFORMATION: Asn (Trt)  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (8)  
; OTHER INFORMATION: Nle  
US-09-442-989-31

Query Match 75.4%; Score 46; DB 4; Length 12;  
Best Local Similarity 75.0%; Pred. No. 0.013;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVSEIQFMNHLG 12  
Db 1 AVSEIQLXNHLG 12

## RESULT 2

US-08-817-547A-1  
; Sequence 1, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03757  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: no  
; ANTI-SENSE: no

US-08-817-547A-1

Query Match 73.8%; Score 45; DB 3; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMN 10  
Db 1 SVSEIQLMHN 10

## RESULT 3

US-08-817-547A-2  
; Sequence 2, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: no  
ANTI-SENSE: no

US-08-817-547A-2

Query Match 63.9%; Score 39; DB 3; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9  
Db 1 SVSEIQLMH 9

## RESULT 4

US-09-421-379-6  
; Sequence 6, Application US/09421379  
; Patent No. 6495662  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald  
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
; FILE REFERENCE: 0609.4570001  
; CURRENT APPLICATION NUMBER: US/09/421,379  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: U.S. 60/105,530  
; EARLIER FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-421-379-6

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Query Match      59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 AVSEIQLMH 9

RESULT 5
US-09-421-379-7
; Sequence 7, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421,379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-421-379-7

Query Match      54.1%; Score 33; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 AVSEIQLLH 9

RESULT 6
US-08-817-547A-3
; Sequence 3, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Adermann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: PCT/EP95/03757
FILING DATE: 29 SEPT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FROST, ROGER T.
REGISTRATION NUMBER: 22,176
REFERENCE/DOCKET NUMBER: 07826-0007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-817-547A-3

Query Match      50.8%; Score 31; DB 3; Length 8;
Best Local Similarity 87.5%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVSEIQFM 8
Db 1 SVSEIQLM 8

RESULT 7
US-09-421-379-10
; Sequence 10, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421,379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-421-379-10

Query Match      47.5%; Score 29; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 SVSEHQLLH 9

RESULT 8
US-08-140-137A-42
; Sequence 42, Application US/08140137A
; Patent No. 5817617
; GENERAL INFORMATION:
; APPLICANT: TUOMANEN, ELAINE
; APPLICANT: MASURE, H. R.
```

us-09-730-174a-4.closed.ra1

Sun Sep 5 09:56:54 2004

;; TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE  
;; TITLE OF INVENTION: ADHESION MOLECULE (BLAM)

;; NUMBER OF SEQUENCES: 49  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSES: Klauber & Jackson  
;; STREET: 411 Hackensack Avenue  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/140,137A  
;; FILING DATE: 27-MAY-1994  
;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 600-1-096  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201 487-5800  
;; TELEFAX: 201 343-1684  
;; TELEX: 133521

;; INFORMATION FOR SEQ ID NO: 42:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; DESCRIPTION: CARD peptide sequence  
;; US-08-140-137A-42

Query Match 47.5%; Score 29; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 23;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSIEIQFMH 9  
Db 5 ISSEQFVH 12

RESULT 9  
5460978-3  
;; Patent No. 5460978  
;; APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,  
;; BRUCE E.; WETTERHALL, RICHARD E.H.  
;; TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL  
;; HYPERCALCEMIA OF MALIGNANCY-PTRHP  
;; NUMBER OF SEQUENCES: 4  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/715,280  
;; FILING DATE: 14-JUN-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 199,235  
;; FILING DATE: 09-MAY-1988  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; SEQ ID NO: 3:  
;; LENGTH: 11  
5460978-3

Query Match 45.9%; Score 28; DB 6; Length 11;  
Best Local Similarity 60.0%; Pred. No. 32;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 10  
Db 1 AVSEHQLEHN 10

RESULT 10  
US-08-817-547A-5  
;; Sequence 5, Application US/08817547A  
;; Patent No. 6030790  
;; GENERAL INFORMATION:  
;; APPLICANT: Adermann, Knut  
;; APPLICANT: Hock, Dieter  
;; APPLICANT: Magerlein, Markus  
;; TITLE OF INVENTION: Peptides from the hPTH Sequence  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jones & Askew, LLP  
;; STREET: 191 Peachtree Street, 37th Floor  
;; CITY: Atlanta  
;; STATE: Georgia  
;; COUNTRY: USA  
;; ZIP: 30303  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/817,547A  
;; FILING DATE:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/EP95/03757  
;; FILING DATE: 29 SEPT 1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: FROST, ROGER T.  
;; REGISTRATION NUMBER: 22,176  
;; REFERENCE/DOCKET NUMBER: 07826-0007  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 404-818-3700  
;; TELEFAX: 404-818-3799  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; HYPOTHEetical: no  
;; ANTI-SENSE: no  
US-08-817-547A-5

Query Match 42.6%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQ 6  
Db 1 SVSEIQ 6

RESULT 11  
US-08-817-547A-4  
;; Sequence 4, Application US/08817547A  
;; Patent No. 6030790  
;; GENERAL INFORMATION:  
;; APPLICANT: Adermann, Knut  
;; APPLICANT: Hock, Dieter  
;; APPLICANT: Magerlein, Markus  
;; TITLE OF INVENTION: Peptides from the hPTH Sequence  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jones & Askew, LLP  
;; STREET: 191 Peachtree Street, 37th Floor  
;; CITY: Atlanta  
;; STATE: Georgia  
;; COUNTRY: USA  
;; ZIP: 30303

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: no
; ANTI-SENSE: no
;
US-08-817-547A-4

Query Match 42.6%; Score 26; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQ 6
Db 1 SVSEIQ 6

RESULT 12
US-09-421-379-8
; Sequence 8, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421,379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-421-379-8

Query Match 42.6%; Score 26; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVSEIQFMH 9
Db 1 AVSEHQLLH 9
```

```

RESULT 13
US-08-482-228-42
; Sequence 42, Application US/08482228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy L.
; APPLICANT: Helgeson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-228-42

Query Match 41.0%; Score 25; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEIQFMH 9
Db 5 SSVTFMH 11

RESULT 14
US-08-482-528-42
; Sequence 42, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy L.
; APPLICANT: Helgeson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
```

CITY: Irvine  
STATE: California  
COUNTRY: USA  
ZIP: 92713-5210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,528  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthrie, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-528-42

Query Match 41.0%; Score 25; DB 3; Length 12;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SEIQFMH 9  
| : |||  
Db 5 SSVTFMH 11

RESULT 15  
US-08-177-109A-56  
Sequence 56, Application US/08177109A  
Patent No. 5869615  
GENERAL INFORMATION:  
APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/177,109A  
FILING DATE: 03-JAN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-177-109A-56  
Query Match 39.3%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 8 MHNIG 12  
| : |||  
Db 1 LHNMG 5  
Search completed: September 5, 2004, 09:38:33  
Job time : 12 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43 ; Search time 9.5 seconds  
(without alignments)  
121.505 Million cell updates/sec

Title: US-09-730-174A-5  
Perfect score: 59  
Sequences: 1 AVSEIQLMNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:  
1: pir1:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	35.6	12	2 S21205	Ig heavy chain V r
2	18	30.5	7	2 A58718	carnocin UI49 - Ca
3	18	30.5	9	2 S78420	ribosomal protein
4	18	30.5	10	2 A60589	sperm-activating p
5	18	30.5	10	2 B46453	e antigen p20e pre
6	18	30.5	12	2 A55837	5-aminimidazole r
7	17	28.8	7	2 I45868	alpha-myosin heavy
8	17	28.8	10	2 A37268	Ig heavy chain C r
9	17	28.8	12	2 PH1190	T-cell receptor al
10	17	28.8	12	2 PH1189	T-cell receptor al
11	17	28.8	12	2 PH1189	T-cell receptor al
12	16	27.1	10	2 A47364	placental lactogen
13	16	27.1	11	2 PH0924	T-cell receptor be
14	15	25.4	7	2 S25266	p11E protein - Bsc
15	15	25.4	7	2 S29735	polyposphate-gluc
16	15	25.4	7	2 S29735	chlorophyll a/b-bi
17	15	25.4	9	2 PW0002	N-methylpurine DNA
18	15	25.4	10	2 A50029	T-cell receptor ga
19	15	25.4	11	2 A38841	rhodopsin homolog
20	15	25.4	11	2 B41835	translation elonga
21	15	25.4	11	2 A40795	glycoprotein H-a -
22	14	23.7	4	2 I38888	COI intron 16 prot
23	14	23.7	7	2 T09512	NADH2 dehydrogenas
24	14	23.7	9	2 PT0238	Ig heavy chain CRD
25	14	23.7	10	1 SPFGNK	neuromedin K - pig
26	14	23.7	10	2 S28055	cytochrome b559 co
27	14	23.7	10	2 S27873	hypothetical prote
28	14	23.7	10	2 C61033	ranatachikin C -
29	14	23.7	11	2 S71304	amine oxidase (cop

30 14 23.7 11 2 S60354 retinal oxidase -  
31 14 23.7 11 2 B29806 acidic proline-ric  
32 14 23.7 11 4 S41909 hypothetical prote  
33 14 23.7 12 2 S25485 transcription fact  
34 14 23.7 12 2 G49410 t-complex polyypept  
35 14 23.7 12 2 S71034 potB protein - Sal  
36 14 23.7 12 2 PH1175 T-cell receptor al  
37 14 23.7 12 2 PH1174 T-cell receptor al  
38 14 23.7 12 2 141235 glutamins-tRNA lig  
39 13 22.0 6 2 PQ0008 angiotensin-conver  
40 13 22.0 8 2 T14906 hypothetical prote  
41 13 22.0 8 2 JS0316 leucokinin VI - Ma  
42 13 22.0 8 2 PH1618 Ig H chain V-D-J r  
43 13 22.0 9 2 S13636 coat protein beta  
44 13 22.0 9 2 JN0026 sperm-activating p  
45 13 22.0 9 2 PT0231 Ig heavy chain CDR

## ALIGNMENTS

## RESULT 1

S21205  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S21205  
R:Makiya, R.; Stigbrand, T.  
Eur. J. Biochem. 205, 341-345, 1992  
A:Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin  
A:Reference number: S21205; MUID:92209522; PMID:1555592  
A:Accession: S21205  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <MAK>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.6%; Score 21; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 6.9e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 EIQLMNLG 12  
|:|:|:|  
Db 1 EVQLVESGG 9

## RESULT 2

A58718  
carnocin UI49 - Carnobacterium sp. (fragment)  
C:Species: Carnobacterium sp.  
C:Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C:Accession: A58718  
R:Stoffeis, G.; Missen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.  
Appl. Environ. Microbiol. 58, 1417-1422, 1992  
A:Title: Purification and characterization of a new bacteriocin isolated from a Carnoba  
A:Reference number: A58718; MUID:92321768; PMID:1622206  
A:Accession: A58718  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <STO>  
C:Keywords: antibiotic; lanthionine

Query Match 30.5%; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6  
|:|:|:|  
Db 2 SEIQ 5

RESULT 3  
S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
 C/Accession: S78420  
 R:Goldschmidt-Reisin, S.; Graack, H.R.  
 submitted to the Protein Sequence Database, February 1998  
 A/Reference number: S78411  
 A/Accession: S78420  
 A/Molecule type: protein  
 A/Residues: 1-9 <GOL>  
 A/Note: the protein is designated as mitochondrial ribosomal protein L41  
 C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 30.5%; Score 18; DB 2; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 HNLG 12  
 Db 5 HRLG 8

RESULT 4  
 A60589  
 sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchin  
 C/Species: Heterocentrotus mamillatus  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
 C/Accession: A60589  
 R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.; Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A/Title: A halogenated amino acid-containing sperm activating peptide and its related polypeptides  
 otus nudus, Echinometrina mathasi and Heterocentrotus mamillatus.  
 A/Reference number: A60527  
 A/Accession: A60589  
 A/Molecule type: protein  
 A/Residues: 1-10 <YOS>  
 C/Superfamily: unassigned animal peptides

Query Match 30.5%; Score 18; DB 2; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12  
 Db 2 YNLG 5

RESULT 5  
 B46453  
 e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)  
 N/Alternate names: HBe antigen precursor  
 N/Contains: e antigen  
 C/Species: hepatitis B virus, HBV  
 A/Variety: subtype adr  
 C/Date: 18-Jun-1993 #sequence\_revision 08-Nov-1996 #text\_change 15-Aug-1997  
 C/Accession: B46453  
 R:Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda, J.; Immunol. 147, 3156-3160, 1991  
 A/Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepatitis B virus  
 A/Reference number: A46453; MUID:92013147; PMID:1717588  
 A/Accession: B46453  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <TAK>  
 A/Experimental source: subtype adr  
 A/Note: sequence extracted from NCBI backbone (NCBIP:60243)  
 F/1-10/Domain: signal sequence (fragment) #status predicted <SIG>

Query Match 30.5%; Score 18; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 IQLMH 9

Db 1 MQLFH 5  
 RESULT 6  
 A55837  
 5-aminoimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminoimidazole  
 C/Species: Gallus gallus (chicken)  
 C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 17-Mar-1999  
 C/Accession: A55837  
 R:Firestone, S.M.; Davissos, V.J.  
 Biochemistry 33, 11917-11926, 1994  
 A/Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal  
 A/Reference number: A55837; MUID:95001903; PMID:7918410  
 A/Accession: A55837  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-12 <FIR>

Query Match 30.5%; Score 18; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVSEIQL 7  
 Db 2 AASELAL 8

RESULT 7  
 I46868  
 alpha-myosin heavy chain - rabbit (fragment)  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
 C/Accession: I46868  
 R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
 A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula  
 A/Reference number: I46868; MUID:84221901; PMID:6328491  
 A/Accession: I46868  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-7 <PRI>  
 A/Cross-references: GB:K01698; NID:gi65538; PIDN:AAA31415.1; PID:gi65539

Query Match 28.8%; Score 17; DB 2; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 QLMHN 10  
 Db 1 QKXHD 5

RESULT 8  
 A37268  
 Ig heavy chain C region (129) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A/Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A/Reference number: A38740; MUID:91177923; PMID:1706720  
 A/Accession: A37268  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-10 <RUF>

Query Match 28.8%; Score 17; DB 2; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 3.3e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 BIQLMHNLG 12

Db 1 ESQSFNVG 9

## RESULT 9

PH1190  
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1190  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: PH1190  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4

|||||

Db 2 AVSE 5

## RESULT 10

PH1187  
T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1187  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: PH1187  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4

|||||

Db 2 AVSE 5

## RESULT 11

PH1189  
T-cell receptor alpha chain V region (Cw3/2C3) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1189  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: PH1189  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSE 4

|||||

Db 2 AVSE 5

## RESULT 12

A47364  
Placental lactogen-I precursor - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C:Accession: A47364  
R:Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.  
Mol. Endocrinol. 7, 181-188, 1993  
A:Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pr  
A:Reference number: A47364; MUID:93225959; PMID:8469232  
A:Accession: A47364  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-10 <RES>  
A:Cross-references: GB:S58124; NID:G299449

Query Match 27.1%; Score 16; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 5.1e+03; 2; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IQLMHL 11

|||||

Db 1 MQLTLN 7

## RESULT 13

PH0924  
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0924  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0924  
A:Molecule type: mRNA  
A:Residues: 1-11 <GOL>  
A:Experimental source: concanavalin A-activated lymphoblast  
C:Keywords: T-cell receptor

Query Match 27.1%; Score 16; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 5.7e+03; 3; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQLM 8

|||||

Db 2 ASSSMDLM 9

## RESULT 14

S25266  
pIIE protein - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C>Date: 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 11-Jun-1993  
C:Accession: S25266  
R:Dupuy, B.; Taha, M.K.; Possot, O.; Marchal, C.; Pugsley, A.P.  
Mol. Microbiol. 6, 1887-1894, 1992  
A:Title: Pulo, a component of the pullulanase secretion pathway of Klebsiella oxytoca,  
A:Reference number: S25266; MUID:92374839; PMID:1354833  
A:Accession: S25266  
A:Molecule type: protein  
A:Residues: 1-7 <DUP>  
C:Genetics:  
A:Gene: pIIE

Query Match 25.4%; Score 15; DB 2; Length 7;

Best Local Similarity 75.0%; Pred. No. 2.8e+05; 1; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

us-09-730-174a-5.closed.rpr

Sun Sep 5 09:56:57 2004

QY 5 IOLM 8  
|:|  
Db 4 IELM 7

RESULT 15

S29735  
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichii  
C;Species: Propionibacterium freudenreichii subsp. shermanii  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002  
C;Accession: S29735  
R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A;Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium shermanii  
A;Reference number: S29735; MUID:93143332; PMID:8380966  
A;Accession: S29735  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <PHI>  
C;Keywords: phosphotransferase

Query Match 25.4%; Score 15; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. NO. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12  
|:|  
Db 2 HVLG 5

Search completed: September 5, 2004, 09:37:44  
Job time : 9.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds  
(without alignments)  
96.130 Million cell updates/sec

Title: US-09-730-174A-5  
Perfect score: 59  
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	30.5	7	1 LANC_CARUI	P36960 carnobacter
2	16	27.1	8	1 ALL6_CVDPO	P82157 cydia pomon
3	16	27.1	8	1 FUSS_FUSSO	P81010 fusarium so
4	16	27.1	11	1 EFG_CLOPA	P81350 clostridium
5	15	25.4	11	1 PVKI_PERAM	P41837 periplaneta
6	14	23.7	6	1 TRPI_PSEPU	P36414 pseudomonas
7	14	23.7	7	1 ALL7_CVDPO	P82158 cydia pomon
8	14	23.7	8	1 ALI8_CARMA	P81821 carcinus ma
9	14	23.7	8	1 ALL1_CVDPO	P82152 cydia pomon
10	14	23.7	9	1 FAR8_MACRS	P83281 macrobrachi
11	14	23.7	9	1 UF02_MOUSE	P38640 mus musculu
12	14	23.7	10	1 ALI9_CARMA	P81822 carcinus ma
13	14	23.7	10	1 PSBF_CAPAN	Q03367 capsicum an
14	14	23.7	10	1 TENK_RANTE	P56923 rana tempor
15	14	23.7	10	1 TRNC_RANCA	P22690 rana catesb
16	14	23.7	10	1 TRNK_PIG	P01292 sus scrofa
17	14	23.7	11	1 ASL1_BACSE	P83146 bacteroides
18	14	23.7	12	1 CD11_LITXA	P58245 litorea xan
19	14	23.7	12	1 CD14_LITXA	P58246 litorea xan
20	14	23.7	12	1 POR8_METTM	P80903 methanobact
21	14	23.7	12	1 RS19_TOBBP	Q56251 tomato big
22	13	22.0	8	1 LCK4_LEUMA	P21143 leucophaea
23	13	22.0	8	1 LCK6_LEUMA	P19988 leucophaea
24	13	22.0	9	1 MOSH_GLYJA	P19852 clypeaster
25	13	22.0	9	1 PPK1_PERAM	P82691 periplaneta
26	13	22.0	10	1 RREL_PHODV	P35946 phocine dis
27	13	22.0	11	1 CS15_BACSU	P81095 bacillus su
28	13	22.0	11	1 Q20A_COMTE	P80464 comamonas t
29	13	22.0	12	1 PPX4_PERFU	P82690 periplaneta
30	12	20.3	9	1 FIBB_PAPHA	P19343 papio hamad
31	12	20.3	9	1 RE42_LITRU	P82075 litorea rub
32	12	20.3	10	1 GLEM_HUMAN	P02728 homo sapien
33	12	20.3	10	1 GONI_CLUPEA	P81749 clupea pall

34 12 20.3 10 1 GON2\_CHEPR P80678 chelyosoma  
35 12 20.3 10 1 HTF1\_ROMMI P81100 romalea mic  
36 12 20.3 10 1 HTF1\_HELZE P16353 heliothis z  
37 12 20.3 10 1 SYK\_CAMUP Q46464 campylobact  
38 12 20.3 10 1 TRNB\_RANRI P29135 rana rigibu  
39 12 20.3 11 1 CXLI\_CONNR P59807 conus marmo  
40 12 20.3 11 1 HS70\_PINPS P81672 pinus pinas  
41 12 20.3 11 1 T2P1\_PROVU P31031 proteus vul  
42 12 20.3 12 1 HEP1\_BACSE P83054 bacteroides  
43 12 20.3 12 1 PPK4\_PERAM P82619 periplaneta  
44 11 18.6 7 1 TY51\_LITRU P82065 litorea rub  
45 11 18.6 7 1 UN06\_PINPS P81675 pinus pinas

## ALIGNMENTS

RESULT 1  
LANC\_CARUI STANDARD; PRT; 7 AA.  
AC P36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin U149 (Fragment).  
OS Carnobacterium sp. (strain U149).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
CX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321769; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).  
CC Active on Gram-positive bacteria.  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 SEIQ 6  
Db 2 SEIQ 5

RESULT 2  
ALL6\_CVDPO STANDARD; PRT; 8 AA.  
ID ALL6\_CVDPO  
AC P82157;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia pomonella 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
CX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Larva;  
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).

CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 Query Match 27.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. NO. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 MNHLG 12  
 Db 3 LYNFG 7  
 RESULT 3  
 FUSS\_FUSSO STANDARD; PRT; 8 AA.  
 ID FUSS\_FUSSO  
 AC P81010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Allergen fus s.13596\* (Fragment).  
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=TARI 3596; TISSUE=Mycelium;  
 RA Verma J., Gangal S.V.;  
 RL Submitted (JUL-1997) to Swiss-Prot.  
 CC -!- ALLERGEN: Causes an allergic reaction in human.  
 KW Allergen.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;  
 Query Match 27.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. NO. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 LMHNL 11  
 Db 3 MSHNV 7  
 RESULT 4  
 EFG\_CLOPA STANDARD; PRT; 11 AA.  
 ID EFG\_CLOPA  
 AC P81350;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (CP 5) (Fragment).  
 GN FUSA.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 sequence analysis of proteins from Clostridium pasteurianum W5."  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of  
 the nascent protein chain from the A-site to the P-site of the  
 ribosome.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPbind.

DR PROSITE; PS00301; EFACTOR GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;  
 Query Match 27.1%; Score 16; DB 1; Length 11;  
 Best Local Similarity 25.0%; Pred. NO. 3.5e+03;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 IQLMNLG 12  
 Db 4 LKFMQIG 11  
 RESULT 5  
 PVK1\_PERAM STANDARD; PRT; 11 AA.  
 ID PVK1\_PERAM  
 AC P41837;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Periviscerokinin-1 (Pea-PVK-1).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE=Abdominal perisymphathetic organs;  
 RX MEDLINE=95232021; PubMed=7716075;  
 RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;  
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the  
 perisymphathetic organs of the American cockroach."  
 RL Peptides 16:61-66(1995).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE  
 HYPERNEURAL MUSCLE.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 11  
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;  
 Query Match 25.4%; Score 15; DB 1; Length 11;  
 Best Local Similarity 50.0%; Pred. NO. 5.5e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 IQLMHN 10  
 Db 6 IPVMRN 11  
 RESULT 6  
 TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 ID TRPI\_PSEPU  
 AC P36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE HTH-type transcriptional regulator trpI (trpBA operon transcriptional  
 activator) (Fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PPG1 C1S;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 putida."  
 RL Biochimie 71:521-531(1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
 CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -!- SIMILARITY: Contains 1 HTH lyase-type DNA-binding domain.  
 CC -----  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC -----  
 CC EMBL; X13299; CAA31660.1; ..  
 CC InterPro; IPR000847; HTH\_Lyase.  
 CC PROSITE; PS09311; HTH\_LYSE; PARTIAL.  
 CC Tryptophan biosynthesis; Transcription regulation; Activator;  
 CC DNA-binding.  
 CC NON\_TER 6  
 CC SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 6;  
 Best Local Similarity 40.0%; Pred.No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 LMHNL 11  
 : : :  
 Db 1 MAHDL 5

## RESULT 7

ALL7\_CVDPO  
 ID ALL7\_CVDPO STANDARD; PRT; 7 AA.  
 AC P82158;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 7.  
 OS Cydia pomonella (Codling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 CC NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7  
 FT SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 7;  
 Best Local Similarity 40.0%; Pred.No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MHNLG 12  
 : : :  
 Db 2 MYDFG 6

## RESULT 8

AL18\_CARMA  
 ID AL18\_CARMA STANDARD; PRT; 6 AA.  
 AC P81821;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 18.

OS Carcinus maenas (Common shore crab) (Green crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 CC Eubrachyura; Portunoidea; Portunidae; Carcinus.  
 CC NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred.No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 MHNLG 12  
 : : :  
 Db 3 MYSFG 7

## RESULT 9

ALL1\_CVDPO  
 ID ALL1\_CVDPO STANDARD; PRT; 8 AA.  
 AC P82152;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 1.  
 OS Cydia pomonella (Codling moth).  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 CC NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred.No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 HNLG 12  
 : : :  
 Db 4 YNFG 7

## RESULT 10

FAR8\_MACRS  
 ID FAR8\_MACRS STANDARD; PRT; 9 AA.  
 AC P83281;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP8 (VSHNNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).

```

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RL eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -|- MASS SPECTROMETRY; MW=1133.8; METHOD=MALDI.
CC -|- SIMILARITY: Belongs to the FAP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;
AMIDATION.

Query Match 23.7%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10
DB 3 HN 4

RESULT 11
UF02_MOUSE STANDARD; PRT; 9 AA.
AC P386f0;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.0, its MW is: 32 kDa.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 23.7%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIQ 6
DB 4 EIQ 6

RESULT 12
AL19_CARMA STANDARD; PRT; 10 AA.
AC P81822;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).

```

```

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -|- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -|- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 10
SQ SEQUENCE 10 AA; 1101 MW; 96687CDSAB569AB1 CRC64;
AMIDATION (POTENTIAL).

Query Match 23.7%; Score 14; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MENLG 12
DB 5 MYSFG 9

RESULT 13
PSBF_CAPAN STANDARD; PRT; 10 AA.
AC Q33367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (fragment).
GN PSBF.
OS Capsicum annuum (Bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -|- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -|- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -|- SIMILARITY: Belongs to the psbE / psbF family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; X65570; CAA46539.1; --
DR FR; S28055; S28055.
DR HAVAP; MF 00643; -.
DR InterPro; IPR006216; Cyt_b559.
DR PROSITE; PS00537; CYTOCHROME B559; PARTIAL.
DR Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1

```

FT TRANSMEM <1 5 BY SIMILARITY  
FT DOVAIN 6 10 LUMENAL (POTENTIAL)  
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D69DC5 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
Best Local Similarity 25.0%; Pred. No. 7.7e+03;  
Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQLM 8  
Db 1 SISAMQFI 8

RESULT 14  
TEMK RANTE STANDARD; PRT; 10 AA.  
AC P56923;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 18-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Temporin K.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Skin secretion;  
RX MEDLINE=97175050; PubMed=9022719;  
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
temporaria.";  
RL Eur. J. Biochem. 242:788-792(1996).  
CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 7.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMHNL 11  
Db 1 LLPNL 5

RESULT 15  
TKNC RANCA STANDARD; PRT; 10 AA.  
AC P22690;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatachykinin C (RTK C).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Intestine;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
brain and intestine.";  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]

RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
evolve behavioral responses, are potent vasodilators and  
secretagogues, and contract (directly or indirectly) many smooth  
muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; C61033; C61033.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1086 MW; 3A3A407059D5BDC7 CRC64;

Query Match 23.7%; Score 14; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HN 10  
Db 1 HN 2

Search completed: September 5, 2004, 09:35:03  
Job time : 6.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds  
(without alignments)  
137.681 Million cell updates/sec

Title: US-09-730-174A-5

Perfect score: 59

Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.\*  
1: sp\_arched.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rviris.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	45.8	11	13 Q9PS71	Q9PS71 agkistrodon
2	23	39.0	12	13 P82081	P82081 limnodynast
3	20	33.9	8	13 P82082	P82082 limnodynast
4	20	33.9	8	13 P82083	P82083 limnodynast
5	20	33.9	12	13 P82085	P82085 limnodynast
6	19	32.2	8	8 Q34909	Q34909 locusta mig
7	19	32.2	9	12 Q92766	Q92766 canine mig
8	19	32.2	9	12 Q71066	Q71066 canine dist
9	18	30.5	8	10 Q40659	Q40659 oryza sativ
10	18	30.5	10	12 Q9PXC3	Q9PXC3 hepatitis b
11	18	30.5	11	5 Q23876	Q23876 dictyosteli
12	18	30.5	12	15 Q85631	Q85631 avian carc
13	17	28.8	7	6 Q28742	Q28742 oryctolagus
14	17	28.8	9	4 Q15891	Q15891 homo sapien
15	17	28.8	9	8 Q9GDI2	Q9GDI2 linospadix
16	17	28.8	9	8 Q9GCV6	Q9GCV6 sclerosperm

17	17	28.8	11	10 P82336	P82336 pisum sativ
18	17	28.8	11	13 Q9PST1	Q9PST1 fugu rubrip
19	16	27.1	8	3 Q05403	Q05403 saccharomyc
20	16	27.1	8	4 Q15894	Q15894 homo sapien
21	16	27.1	9	2 Q44377	Q44377 aeromonas t
22	16	27.1	9	2 Q44468	Q44468 aeromonas v
23	16	27.1	9	2 Q8RKU3	Q8RKU3 borrelia bu
24	16	27.1	9	2 Q43928	Q43928 aeromonas p
25	16	27.1	9	2 Q44001	Q44001 aeromonas e
26	16	27.1	9	2 Q9KAM6	Q9KAM6 staphylococ
27	16	27.1	9	10 Q9FXL0	Q9FXL0 lilium long
28	16	27.1	10	2 Q7WUG1	Q7WUG1 pseudomonas
29	16	27.1	10	10 P82132	P82132 spinacia ol
30	16	27.1	10	10 P82133	P82133 spinacia ol
31	16	27.1	10	13 P82080	P82080 limnodynast
32	16	27.1	12	2 Q9X6Y0	Q9X6Y0 aquifex pyr
33	15	25.4	7	12 Q66205	Q66205 transmissib
34	15	25.4	8	13 P82079	P82079 limnodynast
35	15	25.4	9	2 Q43960	Q43960 azotobacter
36	15	25.4	9	5 Q8WTI9	Q8WTI9 drosophila
37	15	25.4	10	6 Q9TS43	Q9TS43 sus scrofa
38	15	25.4	10	8 Q8WBR7	Q8WBR7 chaitophoru
39	15	25.4	11	6 Q9BDC8	Q9BDC8 pongo pygma
40	15	25.4	11	6 Q9BDQ9	Q9BDQ9 gorilla gor
41	15	25.4	11	6 Q9BDD0	Q9BDD0 pan troglod
42	15	25.4	11	6 Q9BDC9	Q9BDC9 pan paniscu
43	15	25.4	12	6 Q9TOY5	Q9TOY5 bos taurus
44	15	25.4	12	11 Q9EQV3	Q9EQV3 mus musculu
45	14	23.7	8	2 Q49534	Q49534 mycoplasma

## ALIGNMENTS

### RESULT 1

Q9PS71 ID Q9PS71 PRELIMINARY; PRT; 11 AA.  
AC Q9PS71;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Fibrinolytic metalloproteinase (Fragment).  
OS Agkistrodon contortrix.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Agkistrodon.  
CX NCBI\_TaxID=8720;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=91378546; PubMed=1899066;  
RA Guan A.L., Retzius A.D., Henderson G.N., Markland F.S.Jr.;  
RT "Purification and characterization of a fibrinolytic enzyme from venom  
of the southern copperhead snake (Agkistrodon contortrix).";  
RL Arch. Biochem. Biophys. 289:197-207(1991).  
FT NON PER 11 11  
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 45.8%; Score 27; DB 13; Length 11;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 QLMHNLG 12  
:| |||||  
Db 4 ELGNLNG 10

### RESULT 2

P82081 ID P82081 PRELIMINARY; PRT; 12 AA.  
AC P82081;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 3.  
 OS Limnodynastes terraereginae (Northern banjo frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OC NCBI\_TaxID=104894;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and  
 Limnodynastes terraereginae";  
 RL Aust. J. Chem. 46:1833-842(1993).  
 CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70FDF472724 CRC64;

Query Match 39.0%; Score 23; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 1e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 |:|:|  
 Db 6 LNNLG 11

RESULT 3  
 P82082 ID P82082 PRELIMINARY; PRT; 8 AA.  
 AC P82082;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 4.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OC NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri";  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=772; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 |:|:|  
 Db 2 LVSNG 7

RESULT 4  
 P82083 ID P82083 PRELIMINARY; PRT; 8 AA.  
 AC P82083;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 5.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OC NCBI\_TaxID=39404;  
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri";  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=786; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 |:|:|  
 Db 2 LISNLG 7

RESULT 5  
 P82085 ID P82085 PRELIMINARY; PRT; 12 AA.  
 AC P82085;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 7.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OC NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=SKIN SECRETION;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri";  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=1114; METHOD=FAB.  
 SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;

Query Match 33.9%; Score 20; DB 13; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 4.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LMNLG 12  
 |:|:|  
 Db 6 LLNLG 11

RESULT 6  
 Q34909 ID Q34909 PRELIMINARY; PRT; 8 AA.  
 AC Q34909;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Locusta migratoria (Migratory locust).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OC NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=86223478; Pubmed=2836084;  
 RA McCracken A., Unlenbusch I., Geilissen G.;  
 RT "Structure of the cloned locusta migratoria mitochondrial genome:  
 Restriction mapping and sequence of its ND-1 (URF-1) gene";  
 RL Curr. Genet. 11:625-630(1987).  
 DR EMBL: X05286; CAA28905.1; -  
 GO; GO:0005739; C.mitochondrion; IEA.

```

KW Mitochondrion. 1 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 32.2%; Score 19; DB 8; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMH 9
Db :|||
1 MSYIKLKH 8

RESULT 7
O92766 PRELIMINARY; PRT; 9 AA.
ID O92766
AC O92766;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR SWBL; AF026237; AAC09167.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
Db :|||
1 MHN 3

RESULT 8
O71066 PRELIMINARY; PRT; 9 AA.
ID O71066
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog #10757/96;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 32.2%; Score 19; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10
Db :|||
1 MHN 3

RESULT 9
O40659 PRELIMINARY; PRT; 8 AA.
ID O40659
AC O40659;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha-amylase (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91078641; PubMed=2258052;
RA Kunagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA Rodriguez R.L.;
RT "Expression and secretion of rice alpha-amylase by saccharomycers
RT cerevisiae.";
RL Gene 94:209-216(1990).
DR EMBL; M62916; AAA33892.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 30.5%; Score 18; DB 10; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLMHN 11
Db :|||
1 MQVLNNM 7

RESULT 10
O9EXC3 PRELIMINARY; PRT; 10 AA.
ID O9EXC3
AC O9EXC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E antigen P2OE (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE.
RC MEDLINE=92013147; PubMed=1717588;
RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA Okuma H., Tsuda F., Muneoka E., Miyakawa Y., Mayumi M.;
RT "Molecular heterogeneity of e antigen polypeptides in sera from
RT carriers of hepatitis B virus.";
RL J. Immunol. 147:3156-3160(1991).
DR PIR; B46453; B46453.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1238 MW; 485A6B3AE721B9C7 CRC64;

Query Match 30.5%; Score 18; DB 12; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IQLMH 9
Db :|||

```

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Db      1 MQLFH 5

RESULT 11
Q23876
ID      Q23876      PRELIMINARY;      PRT;      11 AA.
AC      Q23876;
DT      01-NOV-1996 (TReMBLrel. 01, Created)
DT      01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT      01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE      Actin 4.
OS      Dictyostelium discoideum (Slime mold).
OC      Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=82260445; PubMed=6286214;
RA      McKeown M., Firtel R.A.;
RT      "Actin multigene family of Dictyostelium.";
RL      Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR      EMBL; K02957; AAA33150.1; -.
DR      EMBL; K02956; AAA33150.1; JOINED.
SQ      SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match      30.5%; Score 18; DB 5; Length 11;
Best Local Similarity 28.6%; Pred. No. 9.9e+03;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      4 EIQLMEN 10
Db      5 DVQALNN 11

RESULT 12
Q85631
ID      Q85631      PRELIMINARY;      PRT;      12 AA.
AC      Q85631;
DT      01-NOV-1996 (TReMBLrel. 01, Created)
DT      01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE      MH2, proviral DNA, myc to 3' LTR (Fragment).
OS      Avian carcinoma virus.
OC      Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX      NCBI_TaxID=11958;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85033920; PubMed=6092695;
RA      Suttrave P., Jansen H.W., Bister K., Rapp U.R.;
RT      "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT      elements with avian sarcoma viruses Y73 and SR-A.";
RL      J. Virol. 52:703-705(1984).
DR      EMBL; K03100; AAA42388.1; -.
FT      NON_TER 1
SQ      SEQUENCE 12 AA; 1466 MW; 7254B884F30736DB CRC64;

Query Match      30.5%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 HNL 11
Db      2 HNL 4

RESULT 13
Q28742
ID      Q28742      PRELIMINARY;      PRT;      7 AA.
AC      Q28742;
DT      01-NOV-1996 (TReMBLrel. 01, Created)
DT      01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE      Alpha-myosin heavy chain (Fragment).
OS      Oryctolagus cuniculus (Rabbit).

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=84221901; PubMed=6328491;
RA      Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA      Rabinowitz M.;
RT      "Characterization of genomic clones specifying rabbit alpha- and beta-
RT      ventricular myosin heavy chains.";
RL      Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR      EMBL; K01698; AAA31415.1; -.
DR      PIR; I46868; I46868. 1
FT      NON_TER 1
SQ      SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match      28.8%; Score 17; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 QLMEN 10
Db      1 QKQMD 5

RESULT 14
Q15891
ID      Q15891      PRELIMINARY;      PRT;      9 AA.
AC      Q15891;
DT      01-NOV-1996 (TReMBLrel. 01, Created)
DT      01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE      (Clone XP2E8B) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RA      Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA      Coolbaugh M.F., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA      Caskey C.T.H.;
RT      "Isolation of chromosome-specific genes by reciprocal probing of
RT      arrayed cDNAs and cosmid libraries.";
RL      Hum. Mol. Genet. 0:0-0(1995).
DR      EMBL; I32131; AAA73881.1; -.
FT      NON_TER 1
SQ      SEQUENCE 9 AA; 1030 MW; E56635A1A33686D1 CRC64;

Query Match      28.8%; Score 17; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 EIQLMENIG 12
Db      1 EHQMKTSLG 9

RESULT 15
Q9GD12
ID      Q9GD12      PRELIMINARY;      PRT;      9 AA.
AC      Q9GD12;
DT      01-MAR-2001 (TReMBLrel. 16, Created)
DT      01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT      01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE      Ribosomal protein S16 (Fragment).
GN      RPS16.
OS      Linospadix monostachya.
OG      Chloroplast.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Arecoidae;

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OC Areceae; Liospadicinae; Liospadix.  
 OX NCBI\_TaxID=131282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Asmussen C.B., Chase M.W.;  
 RT "Coding and noncoding plastid DNA in palm systematics."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ404941; CAC17917.1; -.  
 DR GO; GO:0009507; Chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1106 MW; 1B9236C2C041B50 CRC64;

Query Match 28.8%; Score 17; DB 8; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8  
 :|||  
 Db 6 VQLM 9

Search completed: September 5, 2004, 09:37:00  
 Job time : 27.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds  
(without alignments)  
92.892 Million cell updates/sec

Title: US-09-730-174A-5  
Perfect score: 59  
Sequence: 1 AVSEIQUHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	89.8	11	3	Aay96968 Parathyro
2	50	84.7	11	6	ABG72607 Parathyro
3	50	84.7	12	6	ABG72608 Parathyro
4	46	78.0	10	2	Aar91644 Human par
5	46	78.0	10	3	Aay68767 Amino aci
6	46	78.0	10	4	Aab86219 Human par
7	46	78.0	10	6	ABR44166 Human par
8	45	76.3	9	4	Aab86225 Human par
9	43.5	73.7	11	2	Aay50600 Resin bou
10	43	72.9	9	3	AA501862 PTH(1-14)
11	43	72.9	9	3	AA501862 PTH(1-14)
12	40	67.8	9	2	Aay96966 Parathyro
13	40	67.8	9	3	Aar91645 Human par
14	40	67.8	9	3	AA501863 PTH(1-14)
15	40	67.8	9	3	Aay96981 Parathyro
16	40	67.8	10	4	Aab6220 Human par
17	40	67.8	10	4	Aab96932 Rat parat
18	40	67.8	11	4	Aab96931 Rat parat
19	40	67.8	11	4	Aab96915 Parathyro
20	40	67.8	12	4	AB84770 Parathyro
21	40	67.8	12	4	Aab96914 Parathyro
22	38	64.4	12	4	AAB84769 Parathyro
23	35	59.3	10	2	AAW45785 Parathyro
24	35	59.3	11	1	ABP71484 Parathyro
25	35	59.3	11	4	AA501862 PTH(1-14)

26	35	59.3	11	6	ABP71485 Parathyro
27	35	59.3	11	6	ABP71483 Parathyro
28	35	59.3	12	4	AA501862 PTH(1-14)
29	35	59.3	12	6	ABP71482 Parathyro
30	33	55.9	9	3	AA501864 PTH(1-14)
31	33	55.9	9	3	AA501864 PTH(1-14)
32	33	55.9	9	3	AA501864 PTH(1-14)
33	32	54.2	8	2	AA501862 PTH(1-14)
34	32	54.2	8	2	AA501862 PTH(1-14)
35	32	54.2	8	2	AA501862 PTH(1-14)
36	30	50.8	9	3	AA501866 PTH(1-14)
37	27	45.8	7	2	AA501866 PTH(1-14)
38	27	45.8	7	2	AA501866 PTH(1-14)
39	27	45.8	10	5	ABG98580 F protein
40	27	45.8	10	5	ABG98582 F protein
41	27	45.8	10	5	ABG98581 F protein
42	27	45.8	11	4	ABU54029 Human DNA
43	27	45.8	12	2	AA501866 PTH(1-14)
44	27	45.8	12	2	AA501866 PTH(1-14)
45	27	45.8	12	3	AA501866 PTH(1-14)

ALIGNMENTS

RESULT 1  
AAY96968  
ID AAY96968 standard; peptide; 11 AA.  
XX AC AAY96968;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).  
XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
XX Homo sapiens.  
PN WO200039278-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 30-DEC-1999; 99WO-US0311108.  
XX  
PR 31-DEC-1998; 98US-0114577P.  
XX  
XX (GARD//) GARDELLA T J.  
XX (KRON//) KRONENBERG H M.  
XX (POTT//) POTTS J T.  
XX (JUEP//) JUEPPNER H.  
Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
WPI; 2000-452384/39.

New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammalian conditions characterized by decreases in bone mass.  
Claim 4; Page 92; 119pp; English.  
Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or S-(L) n-R, are new. S is an amino terminal signaling functional domain of parathyroid hormone (PTH); L is a linker molecule present n times (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding portion of PTH (1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor sequence. The new compounds are used for treating mammalian conditions characterized by decreases in bone mass, determining rates of bone reformation, bone resorption and/or bone remodeling, treating diseases and disorders associated with decreased tether1 activity, increasing CAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
CC regular injections to treat osteoporosis

XX Sequence 11 AA;  
SQ  
Query Match 89.8%; Score 53; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0034; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0;  
QY 1 AVSEIQLMNL 11  
DB 1 AVSEIQLMNL 11

RESULT 2  
ABG72607  
ID ABG72607 standard; peptide; 11 AA.  
XX AC ABG72607;  
XX DT 11-FEB-2003 (first entry)  
XX DE Parathyroid hormone antigenic peptide 2-12.  
XX KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
XX KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.

XX OS Homo sapiens.  
XX OS Mus sp.  
XX OS Rattus sp.  
XX OS Bos taurus.  
XX OS Sus scrofa.  
XX OS Canis familiaris.  
XX Key Location/Qualifiers  
FT Misc-difference 6 /label= Leu, Phe

XX US2002110871-A1.  
XX PD 15-AUG-2002.  
XX PF 05-DEC-2000; 2000US-00730174.  
XX PR 05-DEC-2000; 2000US-00730174.  
XX PA (ZAHN/) ZAHRADNIK R J.  
XX PI (LAVI/) LAVIGNE J R.  
XX PI Zahradnik RJ, Lavigne JR;  
XX WPI; 2003-066685/06.  
XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
XX and isolation of antibodies having an affinity to it, useful for  
XX determining bioactive PTH levels in serum, plasma and/or cell culture  
XX media.

XX Claim 1; Page 5; 11pp; English.  
XX The invention relates to a new antigenic peptide for inducing the  
XX formation and isolation of antibodies having an affinity to it, being  
XX formed from the N-terminus of parathyroid hormone (PTH). Also included  
XX are; (1) a method for producing antibodies useful in the determination of  
XX PTH levels in a biological sample comprising: (a) providing at least one  
XX first peptide antigen comprising a peptide fragment of PTH; (b)  
XX administering the first peptide antigen to a host animal to induce  
XX antibody production; (c) monitoring the antibody titre produced; (d)  
XX isolating antisera produced in the host animal; and (e) selecting  
XX antisera from the isolated antisera produced in the host that is capable  
XX of binding to a second peptide antigen; (2) an antibody (ab) produced by

CC the method; and (3) test kits and analytical procedures used for the  
CC determination of bioactive intact PTH utilising (ab). The methods and  
CC compositions of the present invention are useful for determining  
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
CC The antigens, antibodies and methods of the present invention, as  
CC compared to prior art, have the particular advantages of possessing  
CC greater affinity for PTH, and in particular, are designed to have a novel  
CC recognition for amino acid residues extending beyond the first N-terminal  
CC PTH residue, and further have negligible cross-reactivity with the large  
CC non-molecular forms of PTH. PTH levels are an important parameter in  
CC patients suffering from hypercalcaemia, osteoporosis and primary  
CC hyperparathyroidism. The present sequence represents a PTH antigenic  
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
XX canine and bovine PTH  
XX SQ Sequence 11 AA;

Query Match 84.7%; Score 50; DB 6; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VSEIQLMNLG 12  
DB 1 VSEIQLMNLG 11

RESULT 3  
ABG72608  
ID ABG72608 standard; peptide; 12 AA.  
XX AC ABG72608;  
XX DT 11-FEB-2003 (first entry)  
XX DE Parathyroid hormone antigenic peptide 1-12.

XX KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
XX KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.  
XX OS Homo sapiens.  
XX OS Mus sp.  
XX OS Rattus sp.  
XX OS Bos taurus.  
XX OS Sus scrofa.  
XX OS Canis familiaris.

XX Key Location/Qualifiers  
FT Misc-difference 1 /label= Ser, Ala  
FT Misc-difference 7 /label= Leu, Phe  
XX US2002110871-A1.  
XX PD 15-AUG-2002.  
XX PF 05-DEC-2000; 2000US-00730174.  
XX PR 05-DEC-2000; 2000US-00730174.

XX PA (ZAHN/) ZAHRADNIK R J.  
XX PI (LAVI/) LAVIGNE J R.  
XX PI Zahradnik RJ, Lavigne JR;  
XX WPI; 2003-066685/06.  
XX New parathyroid hormone (PTH) antigenic peptide inducing the formation  
XX and isolation of antibodies having an affinity to it, useful for  
XX determining bioactive PTH levels in serum, plasma and/or cell culture  
XX media.  
XX Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
 CC formation and isolation of antibodies having an affinity to it, being  
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are: (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH  
 XX

SQ Sequence 12 AA;

Query Match 84.7%; Score 50; DB 6; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VSEIQMLHNLG 12  
 DB 2 VSEIQMLHNLG 12  
 ||||| |||||

RESULT 4

AAR91644  
 ID AAR91644 standard; peptide; 10 AA.

XX AC AAR91644;

XX 06-NOV-1996 (first entry)

XX Human parathyroid hormone antigenic peptide hPTH 1-10.

XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 KW diagnosis; active hPTH 1-37.

XX Synthetic.

XX DE4434551-A1.

XX 04-APR-1996.

XX 28-SEP-1994; 94DE-04434551.

XX 28-SEP-1994; 94DE-04434551.

XX (FORS/) FORSMANN W.

XX Adermann K, Forssmann W, Hock D, Maegerlein M;

XX WPI; 1996-180391/19.

XX New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 PT generated using them, able to distinguish between active and inactive  
 PT forms of the hormone.

XX Claim 2; Page 4; 5pp; German.

CC The present sequence is a specific example of claimed immunogenic  
 CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 CC terminal alpha-helical region and/or the non-structured region of the  
 CC hormone. Antibodies and their binding fragments generated by injecting an  
 CC animal with the peptides are useful as diagnostic reagents for  
 CC determination of biologically active hPTH(1-37)

SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 2; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.061;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVSEIQLMHN 10  
 DB 1 SVSEIQLMHN 10  
 :|||||

RESULT 5

AAY68767  
 ID AAY68767 standard; peptide; 10 AA.

XX AC AAY68767;

XX 05-MAY-2000 (first entry)

XX Amino acids 1-10 of a parathyroid hormone (PTH).

XX Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
 KW slimming treatment; cellulite; skin firming.

XX Unidentified.

XX WO200004047-A1.

XX 27-JAN-2000.

XX 07-JUL-1999; 99WO-FR001687.

XX 17-JUL-1998; 98FR-00009193.

XX (SEDE-) SEDERMA.

XX Lintner K;

XX WPI; 2000-171243/15.

XX New parathyroid hormone fragment peptides, used as lipolysis stimulants  
 PT in topically applied cosmetic compositions for slimming treatment of  
 PT excessive weight in hips and thighs.

XX Claim 1; Page 8; 18pp; French.

XX The present sequence represents a parathyroid hormone (PTH) fragment,  
 CC comprising amino acids 1-10. Parathyroid hormone fragments of the  
 CC invention have lipolysis stimulating activity (especially when topically  
 CC administered). The lipolytic activity of the peptides is enhanced when  
 CC they are chemically modified to increase their lipophilicity. The  
 CC peptides are used in cosmetic or dermatological compositions for skin  
 CC care. They are especially used for slimming treatment of excessive weight  
 CC in the thighs and hips, in the treatment of cellulite and for skin  
 CC firming

SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 3; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.061;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVSEIQLMHN 10  
 DB 1 SVSEIQLMHN 10  
 :|||||

[illegible]



us-09-730-174a-5.closed.rag

Sun Sep 5 09:56:56 2004

XX PR 22-OCT-1998; 98US-0105530P.  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 XX (JUEP/) JUEPPNER H.  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-339693/29.  
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 XX acids that encode them, useful for treating osteoporosis.  
 XX Disclosure; Page 26; 73pp; English.  
 XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nie; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
 CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterized by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodeling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists  
 XX SQ Sequence 9 AA;  
 Query Match 72.9%; Score 43; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMH 9  
 DB 1 AVSEIQLMH 9  
 RESULT 12  
 AAY96966  
 ID AAY96966 standard; peptide; 9 AA.  
 XX AAY96966;  
 XX 31-OCT-2000 (first entry)  
 XX Parathyroid hormone N-terminal signaling domain (residues 1-9).  
 XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 bone reformation; resorption; remodeling; tether1; osteoporosis.  
 Homo sapiens.  
 WO200039278-A2.  
 06-JUL-2000.  
 30-DEC-1999; 99WO-US031108.  
 31-DEC-1998; 98US-0114577P.  
 (GARD/) GARDELLA T J.  
 (KRON/) KRONENBERG H M.  
 (POTT/) POTTS J T.  
 (JUEP/) JUEPPNER H.  
 Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 WPI; 2000-452384/39.  
 New compound comprising an amino terminal signaling functional domain  
 linked to a carboxy-terminal binding portion of parathyroid hormone for  
 treating mammalian conditions characterized by decreases in bone mass.  
 Claim 4; Page 92; 119pp; English.  
 Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
 -R, are new. S is an amino terminal signaling functional domain of  
 parathyroid hormone (PTH); L is a linker molecule present n times (where  
 n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
 PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 sequence. The new compounds are used for treating mammalian conditions  
 characterized by decreases in bone mass, determining rates of bone  
 reformation, bone resorption and/or bone remodeling, treating diseases  
 and disorders associated with decreased tether1 activity, increasing cAMP  
 in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 non-peptide PTH (claimed). The new compound can be administered by  
 inhalation unlike the large native PTH or PTHrP which avoids the need for  
 regular injections to treat osteoporosis  
 SQ Sequence 9 AA;  
 Query Match 72.9%; Score 43; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSEIQLMH 9  
 DB 1 AVSEIQLMH 9  
 RESULT 12  
 AAR91645  
 ID AAR91645 standard; peptide; 9 AA.  
 XX AAR91645;  
 XX 06-NOV-1996 (first entry)  
 XX Human parathyroid hormone antigenic peptide hPTH 1-9.  
 XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 KW diagnosis; active hPTH 1-37.  
 XX Synthetic.  
 XX DE4434551-A1.  
 XX 04-APR-1996.  
 XX 28-SEP-1994; 94DE-04434551.  
 XX

XX 28-SEP-1994; 94DE-04434551.  
 XX (FORS/) FORSMANN W.  
 XX Adermann K, Forssmann W, Hock D, Maegerlein M;  
 XX WPI; 1996-180391/19.  
 XX  
 XX New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 XX generated using them, able to distinguish between active and inactive  
 XX forms of the hormone.  
 XX  
 XX Claim 2; Page 4; 5pp; German.  
 XX  
 XX The present sequence is a specific example of claimed immunogenic  
 XX peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 XX terminal alpha-helical region and/or the non-structured region of the  
 XX hormone. Antibodies and their binding fragments generated by injecting an  
 XX animal with the peptides are useful as diagnostic reagents for  
 XX determination of biologically active hPTH(1-37)  
 XX  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 67.8%; Score 40; DB 2; Length 9;  
 XX Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AVSEIQLMH 9  
 XX :|||||  
 XX Db 1 SVSEIQLMH 9  
 XX  
 XX RESULT 13  
 XX AAB01863  
 XX ID AAB01863 standard; peptide; 9 AA.  
 XX AC AAB01863;  
 XX  
 XX 11-SEP-2000 (first entry)  
 XX DT  
 XX PTH(1-14)/PTH(1-14)-derived peptide, SEQ ID NO:7.  
 XX  
 XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 XX calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 XX bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
 XX  
 XX Homo sapiens.  
 XX OS Synthetic.  
 XX  
 XX WO200023594-A1.  
 XX  
 XX 27-APR-2000.  
 XX PD  
 XX 20-OCT-1999; 99WO-US024481.  
 XX PF  
 XX 22-OCT-1998; 98US-0105530P.  
 XX PR  
 XX (GARD/) GARDELLA T J.  
 XX PA (KRON/) KRONENBERG H M.  
 XX PA (POTT/) POTTS J T.  
 XX PA (JUEP/) JUEPPNER H.  
 XX  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-339693/29.  
 XX DR  
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 XX acids that encode them, useful for treating osteoporosis.  
 XX PT  
 XX Disclosure; Page 26; 73pp; English.  
 XX PS  
 XX The invention relates to a novel parathyroid hormone (PTH) peptide  
 XX

CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01850), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: Xi-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
 CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterised by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodelling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists  
 XX  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 67.8%; Score 40; DB 3; Length 9;  
 XX Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AVSEIQLMH 9  
 XX :|||||  
 XX Db 1 AVSEIQLMH 9  
 XX  
 XX RESULT 14  
 XX AAY96981  
 XX ID AAY96981 standard; peptide; 9 AA.  
 XX AC AAY96981;  
 XX  
 XX 31-OCT-2000 (first entry)  
 XX DT  
 XX Parathyroid hormone N-terminal signaling domain.  
 XX DE  
 XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 XX KW bone reformation; resorption; remodeling; tether1; osteoporosis.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX WO200039278-A2.  
 XX PN  
 XX 06-JUL-2000.  
 XX PD  
 XX 30-DEC-1999; 99WO-US031108.  
 XX PF  
 XX 31-DEC-1998; 98US-0114577P.  
 XX PR  
 XX (GARD/) GARDELLA T J.  
 XX PA (KRON/) KRONENBERG H M.  
 XX PA (POTT/) POTTS J T.  
 XX PA (JUEP/) JUEPPNER H.  
 XX  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX

XX WPI; 2000-452384/39.  
 XX New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 XX  
 PS Claim 11; Page 93; 119pp; English.  
 XX  
 XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
 CC -R, are new. S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased tether activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX  
 XX Sequence 9 AA;

Query Match 67.8%; Score 40; DB 3; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
 Db 1 SVSEIQLMH 9

RESULT 15  
 AAB86220  
 ID AAB86220 standard; peptide; 9 AA.  
 XX  
 AC AAB86220;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human parathyroid hormone immunogenic peptide SEQ ID 2.  
 XX  
 KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE19961350-A1.  
 XX  
 PD 21-JUN-2001  
 XX  
 PF 17-DEC-1999; 99DE-01061350.  
 XX  
 PR 17-DEC-1999; 99DE-01061350.  
 XX  
 PA (IMMU-) IMMUNDIAGNOSTIK AG.  
 XX  
 PI Armbruster FP;  
 XX  
 XX WPI; 2001-376318/40.  
 XX  
 XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.  
 XX  
 PS Disclosure; Page 3; 10pp; German.  
 XX  
 XX This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody

CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention  
 XX  
 XX Sequence 9 AA;  
 Query Match 67.8%; Score 40; DB 4; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
 Db 1 SVSEIQLMH 9

Search completed: September 5, 2004, 09:34:30  
 Job time : 36.5 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds  
(without alignments)  
116.332 Million cell updates/sec

Title: US-09-730-174A-5  
Perfect score: 59  
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	59	100.0	12	9	US-09-730-174A-5
2	56	94.9	12	9	US-09-730-174A-3
3	55	93.2	11	9	US-09-730-174A-1
4	55	93.2	12	9	US-09-730-174A-6
5	52	88.1	12	9	US-09-730-174A-4
6	51	86.4	11	9	US-09-730-174A-2
7	46	78.0	10	14	US-10-168-185-1
8	45	76.3	9	14	US-10-168-185-7
9	43	72.9	9	14	US-10-192-673-6
10	41	69.5	8	14	US-10-168-185-8
11	40	67.8	9	14	US-10-192-673-7
12	40	67.8	9	14	US-10-168-185-2
13	33	55.9	9	14	US-10-192-673-8
14	32	54.2	8	14	US-10-168-185-3
15	30	50.8	9	14	US-10-192-673-10

16	28	47.5	12	14	US-10-319-130-16
17	27	45.8	7	14	US-10-168-185-4
18	27	45.8	10	16	US-10-432-234A-75
19	27	45.8	10	16	US-10-432-234A-76
20	27	45.8	10	16	US-10-432-234A-77
21	27	45.8	11	16	US-10-391-364-93
22	26	44.1	10	14	US-10-033-741-61
23	25	42.4	9	9	US-09-746-945-6
24	25	42.4	10	16	US-10-432-234A-74
25	25	42.4	11	12	US-09-747-287-185
26	25	42.4	11	12	US-09-874-350A-151
27	24	40.7	10	9	US-09-826-390-27
28	24	40.7	10	16	US-10-264-309-369
29	24	40.7	11	12	US-10-609-217-41
30	24	40.7	11	12	US-10-832-388-41
31	24	40.7	11	12	US-10-651-723-41
32	24	40.7	11	12	US-10-645-761-41
33	24	40.7	11	16	US-10-666-696-41
34	24	40.7	11	16	US-10-653-048-41
35	24	40.7	12	14	US-10-286-457-294
36	23	39.0	6	14	US-10-168-185-5
37	23	39.0	7	14	US-10-286-457-469
38	23	39.0	7	15	US-10-368-280-12
39	23	39.0	7	15	US-10-374-035-12
40	23	39.0	9	9	US-09-894-018-332
41	23	39.0	9	10	US-09-821-734-4
42	23	39.0	9	10	US-09-854-248-11
43	23	39.0	9	12	US-10-253-286-288
44	23	39.0	9	14	US-10-094-693-50
45	23	39.0	9	15	US-10-117-937-249

## ALIGNMENTS

## RESULT 1

US-09-730-174A-5  
; Sequence 5, Application US/09730174A

; Patent No. US20020110871A1

; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.

; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a

; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H

; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A

; CURRENT FILING DATE: 2000-12-05

; NUMBER OF SEQ ID NOS: 12

; SEQ ID NO 5

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-5

Query Match 100.0%; Score 59; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00072;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNLG 12

Db 1 AVSEIQLMHNLG 12

## RESULT 2

US-09-730-174A-3

; Sequence 3, Application US/09730174A

; Patent No. US20020110871A1

; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.

; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a

; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc

; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 3  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
 US-09-730-174A-3

Query Match 94.9%; Score 56; DB 9; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.0025;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 :|||||  
 Db 1 SVSEIQFMHNLG 12

## RESULT 3

US-09-730-174A-1  
 ; Sequence 1, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 1  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
 US-09-730-174A-1

Query Match 93.2%; Score 55; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLG 12  
 :|||||  
 Db 1 VSEIQLMHNLG 11

## RESULT 4

US-09-730-174A-6  
 ; Sequence 6, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 6  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
 US-09-730-174A-6

Query Match 93.2%; Score 55; DB 9; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.0037;  
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 :|||||  
 Db 1 AVSEIQFMHNLG 12

## RESULT 5

US-09-730-174A-4  
 ; Sequence 4, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 4  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
 US-09-730-174A-4

Query Match 88.1%; Score 52; DB 9; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 0.013;  
 Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 1 AVSEIQLMHNLG 12  
 :|||||  
 Db 1 SVSEIQFMHNLG 12

## RESULT 6

US-09-730-174A-2  
 ; Sequence 2, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
 US-09-730-174A-2

Query Match 86.4%; Score 51; DB 9; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.018;  
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 2 VSEIQLMHNLG 12  
 :|||||  
 Db 1 VSEIQFMHNLG 11

## RESULT 7

US-10-168-185-1  
 ; Sequence 1, Application US/10168185  
 ; Publication No. US20030175802A1  
 ; GENERAL INFORMATION:

; APPLICANT: Ambruster, Franz Paul  
 ; APPLICANT: Missbichler, Albert  
 ; APPLICANT: Schmidt-Gayk, Heinrich  
 ; APPLICANT: Roth, Heinz-Jürgen  
 ; TITLE OF INVENTION: Method for Determining Parathormone

; TITLE OF INVENTION: Activity in a Human Sample  
; FILE REFERENCE: HLZ-004US  
; CURRENT APPLICATION NUMBER: US/10/168,185  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: DE 19961350  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-185-1

Query Match 78.0%; Score 46; DB 14; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.13;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHN 10  
| | | | | | | | | |  
Db 1 SVSEIQLMHN 10

RESULT 8  
US-10-168-185-7  
; Sequence 7, Application US/10168185  
; Publication No. US20030175802A1  
; GENERAL INFORMATION:  
; APPLICANT: Armbruster, Franz Paul  
; APPLICANT: Missbichler, Albert  
; APPLICANT: Schmidt-Gayk, Heinrich  
; APPLICANT: Roth, Heinz-Jurgen  
; TITLE OF INVENTION: Method for Determining Parathormone  
; TITLE OF INVENTION: Activity in a Human Sample  
; FILE REFERENCE: HLZ-004US  
; CURRENT APPLICATION NUMBER: US/10/168,185  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: DE 19961350  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-185-7

Query Match 76.3%; Score 45; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHN 10  
| | | | | | | | | |  
Db 1 VSEIQLMHN 9

RESULT 9  
US-10-192-673-6  
; Sequence 6, Application US/10192673  
; Publication No. US20030166838A1  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald  
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
; FILE REFERENCE: 0609.4570002

; CURRENT APPLICATION NUMBER: US/10/192,673  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: U.S. 09/421,379  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
; PRIOR FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-192-673-6

Query Match 72.9%; Score 43; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
| | | | | | | | |  
Db 1 AVSEIQLMH 9

RESULT 10  
US-10-168-185-8  
; Sequence 8, Application US/10168185  
; Publication No. US20030175802A1  
; GENERAL INFORMATION:  
; APPLICANT: Armbruster, Franz Paul  
; APPLICANT: Missbichler, Albert  
; APPLICANT: Schmidt-Gayk, Heinrich  
; APPLICANT: Roth, Heinz-Jurgen  
; TITLE OF INVENTION: Method for Determining Parathormone  
; TITLE OF INVENTION: Activity in a Human Sample  
; FILE REFERENCE: HLZ-004US  
; CURRENT APPLICATION NUMBER: US/10/168,185  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: PCT/EP00/12911  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: DE 19961350  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-168-185-8

Query Match 69.5%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQLMHN 10  
| | | | | | | | | |  
Db 1 SEIQLMHN 8

RESULT 11  
US-10-192-673-7  
; Sequence 7, Application US/10192673  
; Publication No. US20030166838A1  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald  
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)

```

; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-10-192-673-7

```

```

Query Match      67.8%; Score 40; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AVSEIQLMH 9
Db 1 AVSEIQLMH 9

```

```

RESULT 12
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-185-2

```

```

Query Match      67.8%; Score 40; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AVSEIQLMH 9
Db 1 AVSEIQLMH 9

```

```

RESULT 13
US-10-192-673-8
; Sequence 8, Application US/10192673
; Publication No. US2003016838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

```

```

; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-10-192-673-8

```

```

Query Match      55.9%; Score 33; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 AVSEIQLMH 9
Db 1 AVSEIQLMH 9

```

```

RESULT 14
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-185-3

```

```

Query Match      54.2%; Score 32; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AVSEIQLM 8
Db 1 SVSEIQLM 8

```

```

RESULT 15
US-10-192-673-10
; Sequence 10, Application US/10192673
; Publication No. US2003016838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of

```

; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; FILE OF INVENTION: Hormone-Related Peptide (PTH-RP)  
; FILE REFERENCE: 0609 4570002  
; CURRENT APPLICATION NUMBER: US/10/192,673  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: U.S. 09/421,379  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: U.S. 60/105,530  
; PRIOR FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-192-673-10

Query Match 50.8%; Score 30; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. NO. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
Db 1 SVSEHLLH 9

Search completed: September 5, 2004, 09:49:38  
Job time : 32.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:32:03 ; Search time 11 Seconds  
(without alignments)  
56.319 Million cell updates/sec

Title: US-09-730-174A-5

Perfect score: 59

Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/2/aaa/5A-COMB.pep:\*

2: /cgn2\_6/prodata/2/aaa/5B-COMB.pep:\*

3: /cgn2\_6/prodata/2/aaa/6A-COMB.pep:\*

4: /cgn2\_6/prodata/2/aaa/6B-COMB.pep:\*

5: /cgn2\_6/prodata/2/aaa/PTCUTS-COMB.pep:\*

6: /cgn2\_6/prodata/2/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	89.8	12	4	US-09-442-989-31
2	46	78.0	10	3	US-08-817-547A-1
3	43	72.9	9	4	US-09-421-379-6
4	40	67.8	9	3	US-08-817-547A-2
5	40	67.8	9	4	US-09-421-379-7
6	35	59.3	11	6	5460978-3
7	33	55.9	9	4	US-09-421-379-8
8	32	54.2	8	3	US-08-817-547A-3
9	30	50.8	9	4	US-09-421-379-10
10	27	45.8	7	3	US-08-817-547A-4
11	25	42.4	10	2	US-08-428-257A-14
12	25	42.4	11	3	US-08-802-981-124
13	24	40.7	5	2	US-08-177-109A-56
14	24	40.7	5	2	US-08-687-706-56
15	24	40.7	5	3	US-08-817-547A-17
16	24	40.7	6	3	US-08-817-547A-16
17	24	40.7	7	3	US-08-817-547A-15
18	24	40.7	8	2	US-08-748-021-64
19	24	40.7	8	3	US-08-817-547A-14
20	24	40.7	8	3	US-08-974-297-64
21	24	40.7	9	3	US-08-817-547A-13
22	24	40.7	10	3	US-08-817-547A-7
23	24	40.7	11	2	US-08-726-464B-13
24	24	40.7	11	4	US-09-428-082B-41
25	23	39.0	6	3	US-08-817-547A-5
26	23	39.0	7	4	US-09-336-083-12
27	23	39.0	7	4	US-09-557-465D-12

Sequence 6, Appli  
Sequence 6, Appli  
Sequence 42, Appl  
Sequence 271, App  
Sequence 74, Appl  
Sequence 75, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 177, App  
Sequence 177, App  
Sequence 71, Appl  
Sequence 73, Appl  
Sequence 71, Appl  
Sequence 27, Appl  
Sequence 56, Appl  
Sequence 27, Appl  
Sequence 89, Appl  
Sequence 41, Appl  
Sequence 184, App

28 23 39.0 10 3 US-08-396-385-6  
29 23 39.0 10 4 US-09-287-221-6  
30 23 39.0 12 4 US-08-140-137A-42  
31 23 39.0 12 4 US-08-474-349A-271  
32 22 37.3 8 3 US-08-160-604-74  
33 22 37.3 8 3 US-08-160-604-75  
34 22 37.3 8 4 US-09-296-089-10  
35 22 37.3 8 4 US-09-296-089-10  
36 22 37.3 9 4 US-09-551-976-10  
37 22 37.3 11 3 US-08-452-543-177  
38 22 37.3 11 3 US-08-652-877-71  
39 22 37.3 11 3 US-08-160-604-73  
40 22 37.3 11 4 US-08-476-515A-71  
41 22 37.3 11 4 US-09-296-089-27  
42 22 37.3 11 4 US-08-475-955-56  
43 22 37.3 12 4 US-09-551-976-27  
44 22 37.3 12 4 US-08-680-454-89  
45 21 35.6 6 2 US-09-591-694-41  
US-08-621-803-184

#### ALIGNMENTS

##### RESULT 1

US-09-442-989-31  
; Sequence 31, Application US/09442989  
; Patent No. 6569993  
; GENERAL INFORMATION:  
; APPLICANT: Sledeski, Adam W.  
; APPLICANT: Mancel, James J.  
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC  
; FILE REFERENCE: A3113B-US  
; CURRENT APPLICATION NUMBER: US/09/442,989  
; CURRENT FILING DATE: 1999-11-18  
; EARLIER APPLICATION NUMBER: 60/081,897  
; EARLIER FILING DATE: 1998-04-15  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)  
; OTHER INFORMATION: Fmoc-Ala  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (3)  
; OTHER INFORMATION: Ser (OtBu)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (4)  
; OTHER INFORMATION: Glu (OtBu)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (6)  
; OTHER INFORMATION: Gln (Trt)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (9)  
; OTHER INFORMATION: His (Trt)  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (10)  
; OTHER INFORMATION: Asn (Trt)  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (8)  
; OTHER INFORMATION: Nle  
US-09-442-989-31

Query Match 89.8%; Score 53; DB 4; Length 12;  
Best Local Similarity 91.7%; Pred. No. 0.0012;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMNLG 12  
|||||

Db 1 AVSEIQLXNLG 12  
|||||

RESULT 2  
US-08-817-547A-1  
; Sequence 1, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A  
; FILING DATE:  
; PRIOR APPLICATION DATA: PCT/EP95/03757  
; APPLICATION NUMBER: 29 SEPT 1994  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; US-08-817-547A-1

Query Match 78.0%; Score 46; DB 3; Length 10;  
Best Local Similarity 90.0%; Pred. No. 0.019;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMHN 10  
|||||

Db 1 SVSEIQLMHN 10  
|||||

RESULT 3  
US-09-421-379-6  
; Sequence 6, Application US/09421379  
; Patent No. 6495662  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald

; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
; FILE REFERENCE: 0609.4570001  
; CURRENT APPLICATION NUMBER: US/09/421,379  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: U.S. 60/105,530  
; EARLIER FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
; US-09-421-379-6

Query Match 72.9%; Score 43; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
|||||

Db 1 AVSEIQLMH 9  
|||||

RESULT 4  
US-08-817-547A-2  
; Sequence 2, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03757  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; US-08-817-547A-2

```
Query Match      67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AVSEIQLMH 9
DB      1 SVSEIQLMH 9

RESULT 5
US-09-421-379-7
; Sequence 7, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421.379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-7

Query Match      67.8%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AVSEIQLMH 9
DB      1 AVSEIQLH 9

RESULT 6
5460978-3
; Patent No. 5460978
; APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,
; BRUCE E.; WETTENHALL, RICHARD E.H.
; TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
; HYPERCALCEMIA OF MALIGNANCY-PTHrP
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/715,280
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 199,235
; FILING DATE: 09-MAY-1988
; APPLICATION NUMBER:
; FILING DATE:
; SEQ ID NO: 3
; LENGTH: 11
5460978-3

Query Match      59.3%; Score 35; DB 6; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AVSEIQLMH 10
DB      1 AVSEIQLMH 10

RESULT 7
US-09-421-379-8
; Sequence 8, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570001
; CURRENT APPLICATION NUMBER: US/09/421.379
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: U.S. 60/105,530
; EARLIER FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-421-379-8

Query Match      55.9%; Score 33; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AVSEIQLMH 9
DB      1 AVSEIQLH 9

RESULT 8
US-08-817-547A-3
; Sequence 3, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Adermann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-3

Query Match 54.2%; Score 32; DB 3; Length 8;  
Best Local Similarity 87.5%; Pred. No. 3e+05;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQLM 8  
Db 1 SVSEIQLM 8

## RESULT 9

US-09-421-379-10  
Sequence 10, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:  
APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: peptide  
US-09-421-379-10

Query Match 50.8%; Score 30; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQLMH 9  
Db 1 SVSEHQLLH 9

## RESULT 10

US-08-817-547A-4  
Sequence 4, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adernann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta

STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-4

Query Match 45.8%; Score 27; DB 3; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVSEIQL 7  
Db 1 SVSEIQL 7

## RESULT 11

US-08-428-257A-14  
Sequence 14, Application US/08428257A  
Patent No. 5885808  
GENERAL INFORMATION:  
APPLICANT: Spooner, Robert A.  
APPLICANT: Epenetos, A.A.  
TITLE OF INVENTION: Compounds to target cells  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jules E. Goldberg  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,257A  
FILING DATE: 07/05/95  
CLASSIFICATION: 514  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-428-257A-14

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Query Match          42.4%; Score 25; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIOL 7
DB 4 VSEVQL 9
      |||:|
      |||:|

RESULT 12
US-08-802-981-124
; Sequence 124, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1997
; APPLICATION NUMBER: US/08/802,981
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-00030005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
US-08-802-981-124

Query Match          42.4%; Score 25; DB 3; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 QLMHN 10
DB 5 QLLHN 9
      |||:|
      |||:|

RESULT 13
US-08-177-109A-56
; Sequence 56, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-56

Query Match          40.7%; Score 24; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHNIG 12
DB 1 LHNWG 5
      |||:|
      |||:|

RESULT 14
US-08-687-706-56
; Sequence 56, Application US/08687706
; Patent No. 5928692
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
```

REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU 107 DIV  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-687-706-56

Query Match 40.7%; Score 24; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MNLG 12  
DB 1 LHMNG 5

RESULT 15  
US-08-817-547A-17  
Sequence 17, Application US/08817547A  
Patent No. 6030790  
GENERAL INFORMATION:  
APPLICANT: Adermann, Knut  
APPLICANT: Hock, Dieter  
APPLICANT: Magerlein, Markus  
TITLE OF INVENTION: Peptides from the hPTH Sequence  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jones & Askew, LLP  
STREET: 191 Peachtree Street, 37th Floor  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,547A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/03757  
FILING DATE: 29 SEPT 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FROST, ROGER T.  
REGISTRATION NUMBER: 22,176  
REFERENCE/DOCKET NUMBER: 07826-0007  
TELEPHONE: 404-818-3700  
TELEFAX: 404-818-3799  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no  
ANTI-SENSE: no  
US-08-817-547A-17

Query Match 40.7%; Score 24; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12  
DB 1 HNLG 4

Search completed: September 5, 2004, 09:38:33  
Job time : 11 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: September 5, 2004, 09:30:43 ; Search time 9.5 Seconds  
(without alignments)  
121.505 Million cell updates/sec

Title: US-09-730-174A-6  
Perfect score: 61  
Sequence: 1 AVSEIQFMNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	32.8	10	2 S28055	Cytochrome b559 co
2	20	32.8	12	2 PH1187	T-cell receptor al
3	18	29.5	7	2 A58718	Carnocin U149 - Ca
4	18	29.5	9	2 S78420	Ribosomal protein
5	18	29.5	10	2 A60589	Sperm-activating p
6	18	29.5	12	2 PH1190	T-cell receptor al
7	17	27.9	8	2 A05169	Neuropeptide M-I -
8	17	27.9	10	2 A37268	Ig heavy chain C r
9	17	27.9	12	1 A43975	Locustamytotropin -
10	17	27.9	12	2 S21205	Ig heavy chain V r
11	17	27.9	12	2 PH1189	T-cell receptor al
12	16	26.2	7	2 I46868	Hyperrethaloemic
13	16	26.2	10	2 JC1416	Hyperrethaloemic
14	16	26.2	10	2 S09138	Hyperrethaloemic
15	16	26.2	11	2 A32428	Amine oxidase (cop
16	15	24.6	7	2 S23735	Polyposphatase-gluc
17	15	24.6	9	2 PT0231	Ig heavy chain CDR
18	15	24.6	9	2 A56029	N-methylpurine DNA
19	15	24.6	10	2 S33844	Lectin GNL1 alpha
20	15	24.6	10	2 S38304	T-cell receptor ga
21	15	24.6	10	2 E49033	Rhodopsin homolog
22	15	24.6	11	2 A38841	5-aminimidazole r
23	15	24.6	12	2 A58837	T-cell receptor al
24	15	24.6	12	2 PH1174	T-cell receptor be
25	15	24.6	12	2 S51737	Neuropeptide Antho
26	14	23.0	4	2 A35779	Ribosomal protein
27	14	23.0	7	2 S78024	Hyperrethaloemic
28	14	23.0	8	2 S08995	Hyperrethaloemic
29	14	23.0	8	2 A49823	Adipokinetic hormo

ALIGNMENTS

RESULT 1

S28055  
Cytochrome b559 component psbP - pepper chloroplast (fragment)  
C:Species: chloroplast Capsicum annuum (pepper)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-Jun-1999  
C:Accession: S28055  
R:Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.  
Plant Mol. Biol. 20, 1185-1188, 1992  
A:Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occurs in the chloroplast  
A:Reference number: S28055; MUID:93099270; PMID:11463853  
A:Accession: S28055  
A:Molecule type: DNA  
A:Residues: 1-10 <KUN>  
A:Cross-references: EMBL:X65570; NID:g14344; PIDN:CAA46539.1; PID:g415734  
C:Genetics:  
A:Gene: psbP  
A:Genome: chloroplast  
C:Superfamily: cytochrome b559 component F  
C:Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 32.8%; Score 20; DB 2; Length 10;  
Best Local Similarity 37.5%; Pred. No. 7.4e+02;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQPM 8  
Db 1 SISAMQPI 8

RESULT 2

PH1187  
T-cell receptor alpha chain V region (Cw3/IF11) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1187  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; W.  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: PH1187  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 32.8%; Score 20; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 9.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVSEIQF 7  
Db 2 AVSETGF 8

```

RESULT 3
A58718
Carnocin UI49 - Carnobacterium sp. (fragment)
C:Species: Carnobacterium sp.
C:Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C:Accession: A58718
R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A:Title: Purification and characterization of a new bacteriocin isolated from a Carnobac-
A:Reference number: A58718; MUID:1622206
A:Accession: A58718
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <STO>
C:Keywords: antibiotic; lanthionine

Query Match      29.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
DB 2 SEIQ 5

RESULT 4
S78420
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: S78420
R:Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A:Reference number: S78411
A:Accession: S78420
A:Molecule type: protein
A:Residues: 1-9 <GO>
A:Note: the protein is designated as mitochondrial ribosomal protein L41
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match      29.5%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
DB 5 HRLG 8

RESULT 5
A60589
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchin
C:Species: Heterocentrotus mamillatus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60589
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi,
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe-
otus nudus, Echinomera mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: A60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
C:Superfamily: unassigned animal peptides

Query Match      29.5%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNLG 12
DB 2 YNLG 5

```

```

RESULT 6
PH1190
T-cell receptor alpha chain V region (CW3/10.1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1190
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid-
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: PH1190
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>

Query Match      29.5%; Score 18; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIOF 7
DB 2 AVSEHGF 8

RESULT 7
A05169
neuropeptide M-I - American cockroach
C:Species: Periplaneta americana (American cockroach)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C:Accession: A05169
R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas-
A:Reference number: A90118; MUID:85046530; PMID:6548628
A:Accession: A05169
A:Molecule type: protein
A:Residues: 1-8 <WIT>
C:Keywords: neuropeptide

Query Match      27.9%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMHN 10
DB 1 EVNFSN 7

RESULT 8
A37268
Ig heavy chain C region (129) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: A37268
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 268, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: A37268
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-10 <RUF>

Query Match      27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12
DB 1 ESQFPNVG 9

```

## RESULT 9

A43975  
 locustamyotropin - migratory locust  
 N:Alternate names: Lom-MT  
 C:Species: Locusta migratoria (migratory locust)  
 C>Date: 11-Feb-1993 #sequence\_revision 02-Jun-1994 #text\_change 08-Dec-1995  
 C:Accession: A43975  
 R:Schooofs, L.; Holman, G.M.; Hayes, T.K.; Tips, A.; Nachman, R.J.; Vandessande, F.; De Lo  
 Peptides 11, 427-433, 1990  
 A>Title: Isolation, identification and synthesis of locustamyotropin (Lom-MT), a novel h  
 A:Reference number: A43975; MUID:90341077; PMID:1974346  
 A:Accession: A43975  
 A:Molecule type: protein  
 A:Residues: 1-12 <SCH>  
 A>Note: the amino end of this peptide is not blocked  
 A:Note: synthetic locustamyotropin mimics natural locustamyotropin only in the amidated  
 C:Comment: This peptide was shown to stimulate visceral muscle contractions in locust ov  
 C:Superfamily: pyrokinin  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F12/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.9%; Score 17; DB 1; Length 12;  
 Best Local Similarity 45.5%; Pred. No. 3.5e+03;  
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNL 11  
 |||||  
 DB 2 AVFAAQFSPRL 12

## RESULT 10

S21205  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
 C:Accession: S21205  
 R:Makiya, R.; Stigbrand, T.  
 Eur. J. Biochem. 205, 341-345, 1992  
 A>Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-  
 A:Reference number: S21205; MUID:92209522; PMID:1555592  
 A:Accession: S21205  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <VAK>  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 3.5e+03;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12  
 |||||  
 DB 1 EVLVESGG 9

## RESULT 11

PH1189  
 T-cell receptor: alpha chain V region (Cw3/2C3) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C:Accession: PH1189  
 R:Caenova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A>Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A:Reference number: S26512; MUID:92364546; PMID:1380061  
 A:Accession: PH1189  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <CAS>

Query Match 27.9%; Score 17; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AVSE 4  
 |||||  
 DB 2 AVSE 5

## RESULT 12

I46868  
 alpha-myosin heavy chain - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
 C:Accession: I46868  
 R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
 A>Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular  
 A:Reference number: I46868; MUID:84221901; PMID:6328491  
 A:Accession: I46868  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7 <FRI>  
 A:Cross-references: GB:K01698; NID:gi65538; PIDN:AAA31415.1; PID:gi65539

Query Match 26.2%; Score 16; DB 2; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 QFMHN 10  
 |||||  
 DB 1 QKMHD 5

## RESULT 13

JC1416  
 hypertrehalosemic hormone I - stick insect (Carausius morosus)  
 N:Alternate names: neuropeptide Cam-HrTH-I  
 N:Contains: hypertrehalosemic factor II  
 C:Species: Carausius morosus  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: JC1416; S07157  
 R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.  
 Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
 A>Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in  
 A:Reference number: JC1416; MUID:93129188; PMID:1482345  
 A:Accession: JC1416  
 A:Molecule type: protein  
 A:Residues: 1-10 <GAE1>  
 R:Gaede, G.; Rinehart Jr., K.L.  
 Biol. Chem. Hoppe-Seyler 368, 67-75, 1987  
 A>Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacu  
 A:Reference number: S07157; MUID:87157103; PMID:3828078  
 A:Accession: S07157  
 A:Molecule type: protein  
 A:Residues: 2, 2-10 <GAE2>  
 C:Comment: Hypertrehalosemic factor II lacks the tryptophan modification.  
 C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplane  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic ac  
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F1/Binding site: carbohydrate (trp) (covalent) #status experimental  
 F10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12  
 ::|||  
 DB 1 QLTFTFWNG 9

## RESULT 14

S09138

hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)  
 N:Alternate names: Cam-HrTH-II  
 C:Species: Extatosoma tiaratum  
 C>Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
 C:Accession: S09138  
 R:Gaede, G.; Rinehart, K.L.  
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
 A:Reference number: S08995; PMID:90253659; PMID:2340112  
 A:Accession: S09138  
 A:Molecule type: protein  
 A:Residues: 1-10 <GAE>  
 A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 26.2%; Score 16; DB 2; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 4.5e+03; Mismatches 4; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12  
 ..|||  
 DB 1 QLTFTPNWG 9

RESULT 15  
 A32428  
 amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 12-Oct-1989 #sequence\_revision 31-Dec-1993 #text\_change 06-Sep-1996  
 C:Accession: A32428  
 R:van der Meer, R.A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A.  
 Biochem. Biophys. Res. Commun. 159, 726-733, 1989  
 A:Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolat  
 A:Reference number: A32428; PMID:89193662; PMID:2539124  
 A:Accession: A32428  
 A:Molecule type: protein  
 A:Residues: 1-7, 'K', 9-11 <VAN>  
 A>Note: the modified residue thought by the authors to be pyrroloquinoline quinone coval  
 C:Keywords: oxidoreductase; quinoprotein; topaquinone  
 F:8/Modified site: topaquinone (Tyr) #status predicted

Query Match 26.2%; Score 16; DB 2; Length 11;  
 Best Local Similarity 37.5%; Pred. No. 5e+03; Mismatches 3; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 SEIQFMHN 10  
 |::|  
 DB 2 SDAVFTYN 9

Search completed: September 5, 2004, 09:37:44  
 Job time : 9.5 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 CompuGen Ltd.  
 OM protein - protein search, using sw model  
 Run on: September 5, 2004, 09:27:07; Search time 6.5 Seconds  
 (without alignments)  
 96.130 Million cell updates/sec  
 Title: US-09-730-174A-6  
 Perfect score: 61  
 Sequence: 1 AVSEIQFWHNLG 12

Scoring table: BLOSUM62  
 Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0  
 Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	32.8	10	1 PSBF CAPAN	Q03367 capsicum an
2	18	29.5	7	1 LANC CARUI	P36960 carnobacter
3	18	29.5	10	1 HFL1 ROMMI	P81110 romalea mic
4	17	27.9	12	1 LMT1 LOCMI	P22395 locusta mig
5	16	26.2	8	1 ALL6 CYDPO	P82157 cydia pomon
6	16	26.2	10	1 HTF2 CARMO	P11385 carausius m
7	15	24.6	5	1 E103 LITRU	P82099 litoria rub
8	15	24.6	8	1 FUS3 FUSFO	P81010 fusarium so
9	15	24.6	11	1 EFG CLOPA	P81350 clostridium
10	15	24.6	11	1 NURM CANFA	P49820 canis fami
11	14	23.0	4	1 FURN ANTEL	P86707 anthopleura
12	14	23.0	7	1 ALL7 CYDPO	P82158 cydia pomon
13	14	23.0	7	1 TY51 LITRU	P82065 litoria rub
14	14	23.0	8	1 AL18 CARWA	P81821 carcinus ma
15	14	23.0	8	1 ALL1 CYDPO	P82152 cydia pomon
16	14	23.0	8	1 HFL1 PERAM	P04548 periplaneta
17	14	23.0	9	1 PAR8 VACRS	P83281 macrobrachi
18	14	23.0	9	1 UF02 MOUSE	P38640 mus musculu
19	14	23.0	10	1 AL19 CARWA	P81822 carcinus ma
20	14	23.0	10	1 FAR2 PENMO	P83317 penaeus mon
21	14	23.0	10	1 FARC CALVO	P41867 calliphora
22	14	23.0	10	1 TKNK RANCA	P22690 rana catesb
23	14	23.0	10	1 TKNK BIG	P01292 sus scrofa
24	14	23.0	11	1 ASL1 BACSE	P83146 bacteroides
25	14	23.0	12	1 FORD METTM	P80903 methanobact
26	14	23.0	12	1 R319 TOBEP	Q56251 tomato big
27	13	21.3	6	1 TRPI PSEPU	P36414 pseudomonas
28	13	21.3	8	1 HNF TENMO	P25419 tenebrio mo
29	13	21.3	8	1 LCK4 LEUMA	P21143 leucophaea
30	13	21.3	8	1 LCK6 LEUMA	P19988 leucophaea
31	13	21.3	9	1 CONO CONGE	P05486 conus geogr
32	13	21.3	9	1 MOSH CLYUA	P19852 clypeaster
33	13	21.3	9	1 OXYT EISFO	P42998 eisenia foe

## ALIGNMENTS

RESULT 1  
 PSBF CAPAN STANDARD; PRT; 10 AA.  
 ID Q03367; 9 1 PPK1 PERAM P82591 periplaneta  
 AC 003367; 11 1 ASL2 BACSE P83147 bacteroides  
 DT 01-JUN-1994 (Rel. 29, Created) 21.3 21.3 11 1 CORZ PERAM P11496 periplaneta  
 DT 01-JUN-1994 (Rel. 29, Last sequence update) 21.3 21.3 11 1 CS15 BACSU P81095 bacillus su  
 DT 10-OCT-2003 (Rel. 42, Last annotation update) 21.3 21.3 11 1 PVK1 PERAM P41837 periplaneta  
 DE Cytochrome b559 beta subunit (PSII reaction center subunit VI) 21.3 21.3 11 1 Q20A COMTE P80464 comamonas t  
 DE (Fragment). 21.3 21.3 12 1 UKA2 HUMAN P21144 homo sapien  
 GN PSBF 21.3 21.3 5 1 RE21 LITRU P82071 litoria rub  
 OS Capsicum annuum (Bell pepper). 12 19.7 5 1 RE31 LITRU P82072 litoria rub  
 OG Chloroplast. 12 19.7 8 1 ANG2 BOTJA Q10582 bothriops ja  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; 12 19.7 8 1 HTF2 PERAM P04549 periplaneta  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; 12 19.7 9 1 FIBB ERYPA P19346 erythrocebu  
 OC lamids; Solanales; Solanaceae; Capsicum.  
 CX NCBI\_TaxID=4072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;  
 RX MEDLINE=93099270; PubMed=1463853;  
 RA Kuntz M., Camara B., Weil J.-H., Schantz R.;  
 RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA  
 editing also occurs in non-photosynthetic chromoplasts.";  
 RL Plant Mol. Biol. 20:1185-1188(1992).  
 CC -!- FUNCTION: This b-type cytochrome II is tightly associated with the  
 reaction center of photosystem II and possibly is part of the  
 water-oxidation complex.  
 CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.  
 CC -!- SIMILARITY: Belongs to the psbE / psbF family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: X65570; CAA46539.1; --  
 CC PIR: S28055; S28055.  
 CC DR HAVAP; MF\_00643; -; 1.  
 CC DR InterPro; IPR006216; Cyt b559.  
 CC DR PROSITE; PS00537; CYTOCHROME B559; PARTIAL.  
 CC KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.  
 CC FT NON\_TER 1 1  
 CC FT TRANSMEM 6 10 BY SIMILARITY.  
 CC FT DOMAIN <1 5 LUMENAL (POTENTIAL).  
 CC FT SEQUENCE 10 AA; 1180 MW; 817D0F59D6D6DC5 CRC64;  
 Query Match 32.8%; Score 20; DB 1; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+02;  
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AVSEIQFM 8  
 Db 1 SISAMQFI 8

RESULT 2  
LANC\_CARUI  
ID LANC\_CARUI STANDARD; PRT; 7 AA.  
AC P36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin U149 (fragment).  
OS Carnobacterium sp. (strain U149).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
RT a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 3 SEIQ 6  
DB 2 SEIQ 5

RESULT 3  
HTFL\_ROMMI  
ID HTFL\_ROMMI STANDARD; PRT; 10 AA.  
AC P18110;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE RO I (Hypertrehalosaemic factor).  
OS Romalea microptera (lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Romaleidae; Romalea.  
OX NCBI\_TaxID=7007;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Ringhart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
RT the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-688(1988).  
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph of insects.  
CC major carbohydrate in the hemolymph of insects).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / RPCH family.  
CC INTERPRO: IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 10;  
Best Local Similarity 33.3%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 2; Mismatches 4;

QY 4 EIQFMENLG 12  
DB 1 QVNFTPNWG 9  
RESULT 4  
LMT1\_LOCMI  
ID LMT1\_LOCMI STANDARD; PRT; 12 AA.  
AC P22335;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locustamyotropin 1 (LOM-MT-1).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Cediopodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Corpora cardiaca;  
RX MEDLINE=90341077; PubMed=1974346;  
RA Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,  
RA Vandesande F., de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin  
RT (LOM-MT), a novel biologically active insect peptide.";  
RL Peptides 11:427-433(1990).  
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
CC activity).  
CC -!- SIMILARITY: Belongs to the pyrokinin family.  
DR PIR; A43975; A43975; Pyrokinin.  
DR INTERPRO: IPR001484; PYROKININ; 1.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1213 MW; D766C92722D6DDDD CRC64;

Query Match 27.9%; Score 17; DB 1; Length 12;  
Best Local Similarity 45.5%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 6;

QY 1 AVSEIQFMENL 11  
DB 2 AVPAAQFSPRL 12

RESULT 5  
ALL6\_CYDPO  
ID ALL6\_CYDPO STANDARD; PRT; 8 AA.  
AC P82157;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia statin 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysa;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: Belongs to the allatostatin family.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 MENLG 12  
 DB 3 LYNFG 7

RESULT 6  
 ID HTF2\_CARMO STANDARD; PRT; 10 AA.  
 AC P11385;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypertrehalosemic factor II (HTF-II) (HPTH-II) (Hypertrehalosemic  
 DE neuropeptide II).  
 OS Carausius morosus (Indian stick insect), and  
 OS Extatosoma tiaratum (Stick insect).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;  
 OC Heteronemidae; Carausius.  
 OX NCBI\_TaxID=7022, 7024;  
 [1]  
 RN SEQUENCE.  
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=87157103; PubMed=3828078;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structure of the hypertrehalosemic factor II from the  
 RT corpus cardiaca of the Indian stick insect, Carausius morosus,  
 RT determined by fast atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).  
 RN [2]

RP SEQUENCE.  
 RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RT Gronphadorhina portentos, Blattella germanica and Blattella orientalis  
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 RT atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 RN [3]  
 RP CARBOHYDRATE-LINKAGE SITE.  
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=93129188; PubMed=1482345;  
 RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;  
 RT "A tryptophan-substituted member of the AKH/RPCH family isolated from  
 RT a stick insect corpus cardiacaum.";  
 RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).  
 CC -!- FUNCTION: Hypertrehalosemic factors are neuropeptides that  
 CC elevate the level of trehalose in the hemolymph (trehalose is the  
 CC major carbohydrate in the hemolymph of insects).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.  
 CC -!- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.  
 DR PIR; JCI416; JCI416.  
 DR PIR; S09138; S09138.  
 DR INTERPRO; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 C-LINKED (MAN) (PROBABLE).  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 EIQFMHNLG 12

Db 1 QLTFTNWG 9

RESULT 7  
 ID EIO3\_LITRU STANDARD; PRT; 5 AA.  
 AC P82059;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Electrin 3.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5 5 AMIDATION.  
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FMH 9  
 DB 1 FVH 3

RESULT 8  
 ID FUSF\_FUSSO STANDARD; PRT; 8 AA.  
 AC P81010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Allergen Fus s I3596\* (Fragment).  
 OS Fusarium solani (subsp. pisi) (Nectria haematococcol).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=70791;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=TARI 3596; TISSUE=Mycelium;  
 RA Verma J., Gangal S.V.;  
 RL Submitted (JUL-1997) to Swiss-Prot.  
 CC -!- ALLERGEN: Causes an allergic reaction in human.  
 KW Allergen.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11  
 DB 5 HNV 7

RESULT 9  
 EFG\_CLOPA

DR HSC-2DPAGE: P49820; DOG.  
DR InterPro: IPR002023; CmpLx1\_24kDa.  
DR PROSITE: PS01099; COMPLEX1\_24K; PARTIAL.  
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
KW Iron-sulfur; Iron; 2Fe-2S.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1099 MW; 267FS369C72DD8 CRC64;  
  
Query Match 24.6%; Score 15; DB 1; Length 11;  
Best Local Similarity 66.7%; Pred. No. 5.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 FMH 9  
DB 7 FVH 9  
  
RESULT 11  
FLRN ANTEL STANDARD; PRT; 4 AA.  
ID FLRN ANTEL  
AC P58707;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Antho-RNamide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RX MEDLINE=90319122; PubMed=1973541;  
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
RA Reinscheid R.K., Nottacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
RT anemone neuropeptide containing an unusual amino-terminal blocking  
RT group.".  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Neuron specific.  
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.  
DR PIR; A35779; A35779.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 1 1 L-3-PHENYLACTYL.  
FT MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;  
  
Query Match 23.0%; Score 14; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 FMH 10  
DB 1 FLRN 4  
  
RESULT 12  
ALL7 CYDPO STANDARD; PRT; 7 AA.  
ID ALL7 CYDPO  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia statin 7.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricoides; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;

DR HSC-2DPAGE: P49820; DOG.  
DR InterPro: IPR002023; CmpLx1\_24kDa.  
DR PROSITE: PS01099; COMPLEX1\_24K; PARTIAL.  
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
KW Iron-sulfur; Iron; 2Fe-2S.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1099 MW; 267FS369C72DD8 CRC64;  
  
Query Match 24.6%; Score 15; DB 1; Length 11;  
Best Local Similarity 66.7%; Pred. No. 5.1e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 FMH 9  
DB 7 FVH 9  
  
RESULT 11  
FLRN ANTEL STANDARD; PRT; 4 AA.  
ID FLRN ANTEL  
AC P58707;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Antho-RNamide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RX MEDLINE=90319122; PubMed=1973541;  
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
RA Reinscheid R.K., Nottacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
RT anemone neuropeptide containing an unusual amino-terminal blocking  
RT group.".  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Neuron specific.  
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.  
DR PIR; A35779; A35779.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 1 1 L-3-PHENYLACTYL.  
FT MOD\_RES 4 4 AMIDATION.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;  
  
Query Match 23.0%; Score 14; DB 1; Length 4;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 FMH 10  
DB 1 FLRN 4  
  
RESULT 12  
ALL7 CYDPO STANDARD; PRT; 7 AA.  
ID ALL7 CYDPO  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia statin 7.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricoides; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;

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RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -|- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7
SQ SEQUENCE 7 AA; 873 MW; 672879CAB569350 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HNLG 12
DB 2 MYDFG 6

RESULT 13
TV51_LITRU
ID_TY51_LITRU STANDARD; PRT; 7 AA.
AC P82065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -|- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; MW=965; METHOD=PAB.
KW Pyrrolidone carboxylic acid; Amidation; Neuropeptide;
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 7 7
FT MOD_RES 1 1
FT MOD_RES 7 7
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQFMH 9
DB 1 QIPWFH 6

RESULT 14
AL18_CARMA
ID_AL18_CARMA STANDARD; PRT; 8 AA.
AC P81821;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 18.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]

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RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -|- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -|- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 919 MW; C82879D5AB569AB5 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 HNLG 12
DB 3 MYSFG 7

RESULT 15
ALL1_CVDPO
ID_ALL1_CVDPO STANDARD; PRT; 8 AA.
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 1.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -|- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HNLG 12
DB 4 YNFG 7

Search completed: September 5, 2004, 09:35:03
Job time : 6.5 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds  
(without alignments)  
137.681 Million cell updates/sec

Title: US-09-730-174A-6

Perfect score: 61

Sequence: 1 AVSEIQPMHNLG 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacterioph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	24	39.3	11 13 Q9PS71	Q9PS71 agkistrodon
2	19	31.1	8 6 Q9TT78	Q9TT78 canis faml
3	19	31.1	9 12 Q92766	Q92766 canine dist
4	19	31.1	9 12 Q71066	Q71066 canine dist
5	19	31.1	12 13 P82081	P82081 limnodynast
6	18	29.5	8 3 Q13591	Q13591 saccharomyc
7	18	29.5	12 8 Q8MES0	Q8MES0 anoda crist
8	18	29.5	12 15 Q85631	Q85631 avian cardi
9	17	27.9	11 5 Q3876	Q3876 dictyosteli
10	17	27.9	12 13 P82085	P82085 limnodynast
11	16	26.2	7 6 Q28742	Q28742 oryctolagus
12	16	26.2	8 3 Q05403	Q05403 saccharomyc
13	16	26.2	8 10 Q40659	Q40659 oryza sativ
14	16	26.2	8 13 P82082	P82082 limnodynast
15	16	26.2	8 13 P82083	P82083 limnodynast
16	16	26.2	9 2 Q44377	Q44377 aeromonas t

17	16	26.2	9 2 Q44468	Q44468 aeromonas v
18	16	26.2	9 2 Q8RK03	Q8RK03 borrelia bu
19	16	26.2	9 2 Q43928	Q43928 aeromonas p
20	16	26.2	9 2 Q44001	Q44001 aeromonas e
21	16	26.2	9 10 Q9FXL0	Q9FXL0 lilium long
22	16	26.2	10 10 P82132	P82132 spinacia ol
23	16	26.2	10 10 P82133	P82133 spinacia ol
24	16	26.2	11 8 Q9GB68	Q9GB68 elaeis guin
25	16	26.2	11 10 P82336	P82336 pisum sativ
26	15	24.6	8 4 Q15894	Q15894 homo sapien
27	15	24.6	8 8 Q34909	Q34909 locusta mig
28	15	24.6	8 13 Q90493	Q90493 eopsaltria
29	15	24.6	9 2 Q43960	Q43960 azotobacter
30	15	24.6	9 4 Q15891	Q15891 homo sapien
31	15	24.6	9 10 Q8S3C6	Q8S3C6 glycine max
32	15	24.6	9 10 Q9BEC0	Q9BEC0 hordeum vul
33	15	24.6	10 4 Q15342	Q15342 homo sapien
34	15	24.6	10 5 P82222	P82222 bombyx mori
35	15	24.6	10 10 Q8GZC8	Q8GZC8 hordeum vul
36	15	24.6	11 4 Q9C057	Q9C057 homo sapien
37	15	24.6	11 6 Q9BDC8	Q9BDC8 pongo pygma
38	15	24.6	11 6 Q9BDQ9	Q9BDQ9 gorilla gor
39	15	24.6	11 6 Q9BDD0	Q9BDD0 pan troglod
40	15	24.6	11 6 Q9BDC9	Q9BDC9 pan paniscu
41	15	24.6	12 4 Q9UNV5	Q9UNV5 homo sapien
42	14	23.0	7 8 Q99182	Q99182 gnatholebia
43	14	23.0	8 2 Q49534	Q49534 mycoplasma
44	14	23.0	8 12 Q84156	Q84156 orf virus (
45	14	23.0	8 13 Q91098	Q91098 manorina me

#### ALIGNMENTS

RESULT 1

ID Q9PS71 PRELIMINARY; PRT; 11 AA.

AC Q9PS71; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DB Fibrinolytic metalloproteinase (Fragment).

OS Agkistrodon contortrix.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Agkistrodon.

OX NCBI\_TaxID=8720;

RN [1]

RP SEQUENCE.

RX MEDLINE=91378546; PubMed=1898066;

RA Guan A.L., Retzius A.D., Henderson G.N., Markland P.S.Jr.;

RT "Purification and characterization of a fibrinolytic enzyme from venom

of the southern copperhead snake (Agkistrodon contortrix

contortrix).";

RL Arch. Biochem. Biophys. 289:197-207(1991).

FT NON TER 11 11

SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 39.3%; Score 24; DB 13; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12

Db 7 HNLG 10

RESULT 2

ID Q9TT78 PRELIMINARY; PRT; 8 AA.

AC Q9TT78; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DE Thymidylate synthase (Fragment).  
 GN TS.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21015404; PubMed=11130975;  
 RA Brouillette J.A., Andrew J.R., Venta P.J.;  
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence  
 method";  
 RL Mamm. Genome 11:1079-1086 (2000).  
 DR EMBL; AF202073; AAF20918.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 899 MW; 6731A1E059CAA867 CRC64;

Query Match 31.1%; Score 19; DB 6; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMHNL 11  
 Db 4 FIHTL 8

RESULT 3  
 O92766 PRELIMINARY; PRT; 9 AA.

AC O92766;  
 DT 01-NOV-1998 (T-EMBLrel. 08, Created)  
 DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)  
 DE Fusion protein (Fragment).  
 GN F.  
 OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
 OX NCBI\_TaxID=11232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dog #5526/89;  
 RA Liemann H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the  
 proximal coding part of the F gene of wild-type and vaccine distemper  
 morbilliviruses";  
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF026237; AAC09167.1; -.  
 FT NON\_TER 9  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10  
 Db 1 MHN 3

RESULT 4  
 O71066 PRELIMINARY; PRT; 9 AA.

ID O71066  
 AC O71066;  
 DT 01-AUG-1998 (T-EMBLrel. 07, Created)  
 DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DE Fusion protein (Fragment).  
 GN F.  
 OS Canine distemper virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
 OX NCBI\_TaxID=11232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dog #10757/96;  
 RA Liemann H., Harder T., Haas L.;  
 RT "Genetic analysis of the central untranslated genome region and the  
 proximal coding part of the F gene of wild-type and vaccine distemper  
 morbilliviruses";  
 RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF026234; AAC09164.1; -.  
 FT NON\_TER 9  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 31.1%; Score 19; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 10  
 Db 1 MHN 3

RESULT 5  
 P82081 PRELIMINARY; PRT; 12 AA.

ID P82081  
 AC P82081;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)  
 DE DYNASTIN 3.  
 OS Limnodynastes terraereginae (Northern banjo frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OX NCBI\_TaxID=104894;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RC TISSUE=TRIAL GLAND.  
 RA Rattery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 the banjo frogs Limnodynastes terrestris, Limnodynastes dumerilii and  
 Limnodynastes terraereginae";  
 RL Aust. J. Chem. 46:833-842 (1993).  
 CC -1- MASS SPECTROMETRY: MW=1236; METHOD=FAE.  
 SQ SEQUENCE 12 AA; 1236 MW; 147AA70EDF472724 CRC64;

Query Match 31.1%; Score 19; DB 13; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHN 12  
 Db 7 LNNLG 11

RESULT 6  
 O13591 PRELIMINARY; PRT; 8 AA.

ID O13591  
 AC O13591;  
 DT 01-JAN-1998 (T-EMBLrel. 05, Created)  
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)  
 DE ORF YNL337M (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Obermaier B., Piravandi E., Rinke M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE FROM N.A.
RA MTPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CAA36271.2; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;

Query Match      29.5%; Score 18; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FMHN 10
DB 4 FMHN 7

RESULT 7
Q8MESO PRELIMINARY; PRT; 12 AA.
AC Q8MESO;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Anoda cristata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Anoda.
OX NCBI_TaxID=183227;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384567; AAM50405.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1431 MW; 9A5E59B65452C9CA CRC64;

Query Match      29.5%; Score 18; DB 8; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 EIQFMHNL 11
DB 3 EPDFVNNI 10

RESULT 8
Q85631 PRELIMINARY; PRT; 12 AA.
AC Q85631;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MH2, proviral DNA, myc to 3' LTR (Fragment).
OS Avian carcinoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11958;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85033920; PubMed=6092695;
RX Suttrave P., Jansen H.W., Bister K., Rapp U.R.;
RT "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT elements with avian sarcoma viruses Y73 and SR-A.";
RL J. Virol. 52:703-705(1984).
DR EMBL; K03100; AAA42388.1; -.
FT NON_TER 1

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SQ SEQUENCE 12 AA; 1466 MW; 72B4B884F30736DB CRC64;

Query Match      29.5%; Score 18; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HNL 11
DB 2 HNL 4

RESULT 9
Q23876 PRELIMINARY; PRT; 11 AA.
AC Q23876;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=82260445; PubMed=6286214;
RA McKeown W., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL; K02957; AAA33150.1; -.
DR EMBL; K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CRC64;

Query Match      27.9%; Score 17; DB 5; Length 11;
Best Local Similarity 28.6%; Pred. No. 1.6e+04;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 EIQFMHN 10
DB 5 DVQALNN 11

RESULT 10
P82085 PRELIMINARY; PRT; 12 AA.
ID P82085
AC P82085;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE DYNASTIN 7.
OS Limnodynastes salmini (Salmin's-striped frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=39404;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs: The structure of the dynastins from
RT Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993).
CC -|- MASS SPECTROMETRY; MW=1114; METHOD=FAB.
SQ SEQUENCE 12 AA; 1114 MW; 3AB5A976CAA72728 CRC64;

Query Match      27.9%; Score 17; DB 13; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+04;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 AVSEIQFMHNLG 12
DB 2 AVSGL--LTVNLG 11

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## RESULT 11

Q28742 ID Q28742 PRELIMINARY; PRT; 7 AA.  
 AC Q28742; 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Alpha-myosin heavy chain (Fragment).  
 DE Oryzotagus cuculus (Rabbit).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=84221901; PubMed=6328491;  
 RX Friedman D.J., Umeda P.K., Sinha A.M., Hau H.-J., Jokovic S.,  
 RA Rabinowitz M.;  
 RT "Characterization of genomic clones specifying rabbit alpha- and beta-  
 RT ventricular myosin heavy chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).  
 DR EMBL; K01698; AAA31415.1; -.  
 DR FIR; I46868; I46868.  
 FT NON TER 1 1  
 SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match 26.2%; Score 16; DB 6; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 QFMHN 10

Db 1 QXHD 5

## RESULT 12

Q05403 ID Q05403 PRELIMINARY; PRT; 8 AA.  
 AC Q05403;  
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)  
 DE DNA for ORF's from chromosome XV (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=FY1679;  
 RX MEDLINE=96021609; PubMed=8533473;  
 RA Zumstein E., Pearson B.M., Kalogetopoulos A., Schweizer M.;  
 RT "A 29,425 kb segment on the left arm of yeast chromosome XV contains  
 RT more than twice as many unknown as known open reading frames.";  
 RL Yeast 11:975-986(1995).  
 DR EMBL; X83121; CAA58183.1; -.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 26.2%; Score 16; DB 3; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHNL 11

Db 2 IHNV 5

## RESULT 13

Q40659 ID Q40659 PRELIMINARY; PRT; 8 AA.  
 AC Q40659;  
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)  
 DE Alpha-amylase (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=4530;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=91078641; PubMed=2258052;  
 RX Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,  
 RA Rodriguez R.L.;  
 RT "Expression and secretion of rice alpha-amylase by saccharomycetes  
 RT cerevisiae.";  
 RL Gene 94:209-216(1990).  
 DR EMBL; M62916; AAA33892.1; -.  
 DR Gramene; Q40659; -.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;

Query Match 26.2%; Score 16; DB 10; Length 8;  
 Best Local Similarity 28.8%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQFMNL 11

Db 1 MQVLNNM 7

## RESULT 14

P82082 ID P82082 PRELIMINARY; PRT; 8 AA.  
 AC P82082;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)  
 DE DYNASTIN 4.  
 OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.  
 OC NCBI\_TaxID=39404;  
 RN [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RP TISSUE=SKIN SECRETION;  
 RX Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RA "Peptides from Australian frogs. The structure of the dynastins from  
 RA Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY: MW=772; METHOD=FAB.  
 SQ SEQUENCE 8 AA; 772 MW; 7B5877245A2C728 CRC64;

Query Match 26.2%; Score 16; DB 13; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+06; 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12

Db 5 NLG 7

## RESULT 15

P82083 ID P82083 PRELIMINARY; PRT; 8 AA.  
 AC P82083;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)  
 DE DYNASTIN 5.

OS Limnodynastes salmini (Salmin's-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Limnodynastinae; Limnodynastes.

OX NCBI\_TaxID=39404;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=SKIN SECRETION;  
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. The structure of the dynastins from  
RL Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";  
RL Aust. J. Chem. 46:1235-1244(1993).  
CC -!- MASS SPECTROMETRY; MW=786; METHOD=FAB.  
SQ SEQUENCE 8 AA; 786 MW; 7B58772455B05728 CRC64;  
  
Query Match 26.2%; Score 16; DB 13; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 NLG 12  
   |||  
Db 5 NLG 7  
  
Search completed: September 5, 2004, 09:37:01  
Job time : 28.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds  
(without alignments)  
92.892 Million cell updates/sec

Title: US-09-730-174A-6  
Perfect score: 61  
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	82.0	11	6	ABG72607 Parathyro
2	50	82.0	12	6	ABG72608 Parathyro
3	49	80.3	11	3	AAY96968 Parathyro
4	42	68.9	10	2	AAR91644 Human par
5	42	68.9	10	3	AAY68767 Amino aci
6	42	68.9	10	4	ABE86219 Human par
7	42	68.9	10	6	ABR44166 Human par
8	41.5	68.0	11	2	AAY50600 Resin bou
9	41	67.2	9	4	AAE86225 Human par
10	39	63.9	9	3	AAE01862 PTH(1-14)
11	39	63.9	9	3	AAY96966 Parathyro
12	36	59.0	9	2	AAR91645 Human par
13	36	59.0	9	3	AAE01863 PTH(1-14)
14	36	59.0	9	3	AAY96981 Parathyro
15	36	59.0	9	4	AAE86220 Human par
16	36	59.0	10	4	AAE96932 Rat parat
17	36	59.0	11	4	AAE96931 Rat parat
18	36	59.0	11	4	AAE96915 Parathyro
19	36	59.0	11	4	AAE84770 Parathyro
20	36	59.0	12	4	AAE96914 Parathyro
21	36	59.0	12	4	AAE84769 Parathyro
22	34	55.7	12	2	AAW45785 Parathyro
23	31	50.8	10	6	ABP71484 Parathyro
24	31	50.8	11	1	AAE82547 (Asn10, T
25	31	50.8	11	4	AAE96892 Rat parat

26	31	50.8	11	6	ABP71485
27	31	50.8	11	6	ABP71483
28	31	50.8	12	4	AAE96891
29	31	50.8	12	6	ABP71482
30	29	47.5	9	3	AAE01864
31	29	47.5	9	3	AAE01864
32	29	47.5	9	3	AAE01864
33	28	45.9	8	2	AAE97062
34	28	45.9	8	2	AAE91646
35	28	45.9	8	4	AAE07467
36	28	45.9	8	4	AAE86221
37	27	44.3	10	4	AAE63991
38	27	44.3	11	4	ABU54029
39	27	44.3	12	2	AAE90421
40	27	44.3	12	2	AAE55148
41	26	42.6	7	3	AAE86894
42	26	42.6	9	3	AAE00068
43	25	41.0	9	3	AAE01866
44	25	41.0	9	6	ABP83654
45	25	41.0	9	6	ABP89380
					ABP88771

ALIGNMENTS

RESULT 1  
ABG72607  
ID ABG72607 standard; peptide; 11 AA.  
XX AC ABG72607;  
XX AC

DT 11-FEB-2003 (first entry)  
XX AC

DE Parathyroid hormone antigenic peptide 2-12.  
XX AC

XX Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;  
KW Primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.  
XX AC

OS Homo sapiens.  
OS Mus sp.  
OS Rattus sp.  
OS Bos taurus.  
OS Sus scrofa.  
XX Canis familiaris.  
XX AC

Key Location/Qualifiers  
FT Misc-difference /label= Leu, Phe  
XX AC

US2002110871-A1.  
XX AC

15-AUG-2002.  
XX AC

05-DEC-2000; 2000US-00730174.  
XX AC

05-DEC-2000; 2000US-00730174.  
XX AC

(ZAHRA) ZAHRADNIK R J.  
(LAVI) LAVIGNE J R.  
XX AC

Zahradnik RJ, Lavigne JR;  
XX AC

WPI; 2003-066685/06.  
XX AC

New parathyroid hormone (PTH) antigenic peptide inducing the formation  
and isolation of antibodies having an affinity to it, useful for  
determining bioactive PTH levels in serum, plasma and/or cell culture  
media.  
XX AC

Claim 1; Page 5; lipp; English.  
XX AC

The invention relates to a new antigenic peptide for inducing the  
formation and isolation of antibodies having an affinity to it, being  
XX AC

CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are: (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH

XX Sequence 11 AA;

Query Match 82.0%; Score 50; DB 6; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQPMHNLG 12

Db 1 VSEIQPMHNLG 11

RESULT 2  
 ABG72608  
 ID ABG72608 standard; peptide; 12 AA.

XX Mus sp.

AC Rattus sp.

DT Bos taurus.

XX Sus scrofa.

XX Canis familiaris.

XX Homo sapiens.

XX Mus sp.

XX Rattus sp.

XX Bos taurus.

XX Sus scrofa.

XX Canis familiaris.

XX Homo sapiens.

XX Mus sp.

XX Rattus sp.

XX Bos taurus.

XX Sus scrofa.

XX Canis familiaris.

XX Homo sapiens.

XX Mus sp.

XX Rattus sp.

XX WPI; 2003-066685/06.  
 DR New parathyroid hormone (PTH) antigenic peptide inducing the formation  
 XX of antibodies having an affinity to it, useful for  
 PT determining bioactive PTH levels in serum, plasma and/or cell culture  
 PT media.

XX Claim 2; Page 5; 11pp; English.

XX The invention relates to a new antigenic peptide for inducing the  
 CC formation and isolation of antibodies having an affinity to it, being  
 CC formed from the N-terminus of parathyroid hormone (PTH). Also included  
 CC are: (1) a method for producing antibodies useful in the determination of  
 CC PTH levels in a biological sample comprising: (a) providing at least one  
 CC first peptide antigen comprising a peptide fragment of PTH; (b)  
 CC administering the first peptide antigen to a host animal to induce  
 CC antibody production; (c) monitoring the antibody titre produced; (d)  
 CC isolating antisera produced in the host animal; and (e) selecting  
 CC antisera from the isolated antisera produced in the host that is capable  
 CC of binding to a second peptide antigen; (2) an antibody (ab) produced by  
 CC the method; and (3) test kits and analytical procedures used for the  
 CC determination of bioactive intact PTH utilising (ab). The methods and  
 CC compositions of the present invention are useful for determining  
 CC bioactive intact PTH levels in serum, plasma and/or cell culture media.  
 CC The antigens, antibodies and methods of the present invention, as  
 CC compared to prior art, have the particular advantages of possessing  
 CC greater affinity for PTH, and in particular, are designed to have a novel  
 CC recognition for amino acid residues extending beyond the first N-terminal  
 CC PTH residue, and further have negligible cross-reactivity with the large  
 CC non-molecular forms of PTH. PTH levels are an important parameter in  
 CC patients suffering from hypercalcaemia, osteoporosis and primary  
 CC hyperparathyroidism. The present sequence represents a PTH antigenic  
 CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,  
 CC canine and bovine PTH

XX Sequence 12 AA;

Query Match 82.0%; Score 50; DB 6; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQPMHNLG 12

Db 2 VSEIQPMHNLG 12

RESULT 3  
 AAY96968  
 ID AAY96968 standard; peptide; 11 AA.

XX AAY96968;

DT 31-OCT-2000 (first entry)

DE Parathyroid hormone N-terminal signaling domain (residues 1-11).

XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 KW bone reformation; resorption; remodeling; tether1; osteoporosis.

XX Homo sapiens.

XX WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.

XX 31-DEC-1998; 96US-0114577P.

XX (GARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POTT/) POTTS J T.

PA (JUEP/) JUEPPNER H.  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
PI WPI; 2000-452384/39.  
XX  
XX New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
XX Claim 4; Page 92; 119pp; English.  
XX  
XX Compounds of the structure or formula S-(L) n-B, R<sub>1</sub>-S-(L) n-R or S-(L) n  
-R, are new. S is an amino terminal signaling functional domain of  
CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
CC sequence. The new compounds are used for treating mammalian conditions  
CC characterized by decreases in bone mass, determining rates of bone  
CC reformation, bone resorption and/or bone remodeling, treating diseases  
CC and disorders associated with decreased tether activity, increasing cAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
XX regular injections to treat osteoporosis  
XX  
XX Sequence 11 AA;  
SQ  
Query Match 80.3%; Score 49; DB 3; Length 11;  
Best Local Similarity 90.9%; Pred. No. 0.02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVSEIQFMNHL 11  
Db ||||| |||||  
1 AVSEIQLMHN 11  
RESULT 4  
AAR91644  
ID AAR91644 standard; peptide; 10 AA.  
XX  
XX AAR91644;  
XX  
XX 06-NOV-1996 (first entry)  
XX  
XX Human parathyroid hormone antigenic peptide hPTH 1-10.  
DE  
XX Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
KW diagnosis; active hPTH 1-37.  
XX  
XX Synthetic.  
XX  
XX DE4434551-A1.  
XX  
XX 04-APR-1996.  
XX  
XX 28-SEP-1994; 94DE-04434551.  
XX  
XX 28-SEP-1994; 94DE-04434551.  
XX  
XX (FORS/) FORSMANN W.  
XX  
XX Adermann K, Forssmann W, Hock D, Maegerlein M;  
PI  
XX WPI; 1996-180391/19.  
XX  
XX New antigenic peptide(s) from human parathyroid hormone - and antibodies  
PT generated using them, able to distinguish between active and inactive  
PT forms of the hormone.  
XX  
XX Claim 2; Page 4; 5pp; German.  
XX

CC The present sequence is a specific example of claimed immunogenic  
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-  
CC terminal alpha-helical region and/or the non-structured region of the  
CC hormone. Antibodies and their binding fragments generated by injecting an  
CC animal with the peptides are useful as diagnostic reagents for  
CC determination of biologically active hPTH(1-37)  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 68.9%; Score 42; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.37;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVSEIQFMHN 10  
Db :||||| |||||  
1 SVSEIQLMHN 10  
RESULT 5  
AAY68767  
ID AAY68767 standard; peptide; 10 AA.  
XX  
XX AAY68767;  
XX  
XX 05-MAY-2000 (first entry)  
XX  
XX Amino acids 1-10 of a parathyroid hormone (PTH).  
DE  
XX Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;  
KW slimming treatment; cellulite; skin firming.  
XX  
XX Unidentified.  
OS  
XX WO200004047-A1.  
XX  
XX 27-JAN-2000.  
XX  
XX 07-JUL-1999; 99WO-FR001687.  
XX  
XX 17-JUL-1998; 98FR-00009193.  
XX  
XX (SEDE-) SEDERMA.  
XX  
XX Lintner K;  
XX  
XX WPI; 2000-171243/15.  
XX  
XX New parathyroid hormone fragment peptides, used as lipolysis stimulants  
PT in topically applied cosmetic compositions for slimming treatment of  
PT excessive weight in hips and thighs.  
XX  
XX Claim 1; Page 8; 18pp; French.  
XX  
XX The present sequence represents a parathyroid hormone (PTH) fragment,  
CC comprising amino acids 1-10. Parathyroid hormone fragments of the  
CC invention have lipolysis stimulating activity (especially when topically  
CC administered). The lipolytic activity of the peptides is enhanced when  
CC they are chemically modified to increase their lipophilicity. The  
CC peptides are used in cosmetic or dermatological compositions for skin  
CC care. They are especially used for slimming treatment of excessive weight  
CC in the thighs and hips, in the treatment of cellulite and for skin  
CC firming  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 68.9%; Score 42; DB 3; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.37;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVSEIQFMHN 10  
Db :||||| |||||  
1 SVSEIQLMHN 10

04-AUG-2003 (first entry)  
 DT XX Human parathyroid hormone (hPTH) fragment (residues 1-10).  
 DE XX Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;  
 XX KW lipolysis; human; hPTH.  
 XX KW Homo sapiens.  
 OS XX WO2003035697-A1.  
 FN XX 01-MAY-2003.  
 XX PD 06-MAY-2002; 2002WO-KR000835.  
 XX PF 27-SEP-2001; 2001KR-00060245.  
 XX PR 15-MAR-2002; 2002KR-00014062.  
 XX PA (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.  
 XX PI Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;  
 XX PI Chang M;  
 XX DR WPI; 2003-468288/44.  
 XX XX Novel fusion peptide comprising self cell-penetrating Tat peptide bound  
 PT to human parathyroid hormone-derived peptide, useful as component of skin  
 PT slimming cosmetic composition.  
 XX DS Claim 5; Page 6; 32pp; English.  
 XX CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-  
 CC penetrating Tat peptide is bound to human parathyroid hormone-derived  
 CC peptide (hPTHDP). The fusion peptide is useful as a component of skin  
 CC slimming cosmetic composition. The fusion peptide does not cause  
 CC irritation, easily and safely penetrates into integument and endothelium,  
 CC does not cause skin disease and has superior lipolysis effects, and is  
 CC durable. The present sequence represents a human parathyroid hormone  
 CC (hPTH) fragment that can be used to construct the fusion peptide  
 XX SQ Sequence 10 AA;  
 Query Match 68.3%; Score 42; DB 6; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 0.37;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 AVSEIQPMHN 10  
 :|||||  
 Db 1 SVSEIQLMHN 10  
 :|||||  
 RESULT 8  
 AAY50600  
 ID AAY50600 standard; peptide; 11 AA.  
 XX AC AAY50600;  
 XX DT 09-FEB-2000 (first entry)  
 XX DE Resin bound cyclic peptide 33.  
 XX KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;  
 KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;  
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;  
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "FMOC-Ala"  
 FT Misc-difference 3 /note= "Ser (OtBu)"

RESULT 6  
 AAB86219  
 ID AAB86219 standard; peptide; 10 AA.  
 AC AAB86219;  
 XX DT 03-SEP-2001 (first entry)  
 XX DE Human parathyroid hormone immunogenic peptide SEQ ID 1.  
 XX KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.  
 XX OS Homo sapiens.  
 XX DE19961350-A1.  
 XX PD 21-JUN-2001.  
 XX PF 17-DEC-1999; 99DE-01061350.  
 XX PR 17-DEC-1999; 99DE-01061350.  
 XX PA (IMMU-) IMMUNODIAGNOSTIK AG.  
 XX PI Armbruster FP;  
 XX DR WPI; 2001-376318/40.  
 XX XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.  
 XX DS Disclosure; Page 3; 10pp; German.  
 XX CC This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody  
 CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 the invention  
 XX SQ Sequence 10 AA;  
 Query Match 68.3%; Score 42; DB 4; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 0.37;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 AVSEIQPMHN 10  
 :|||||  
 Db 1 SVSEIQLMHN 10  
 :|||||  
 RESULT 7  
 ABR44166  
 ID ABR44166 standard; peptide; 10 AA.  
 XX AC ABR44166;  
 XX AC

FT	Misc-difference 4	/note= "Glu(OtBu)"
FT	Misc-difference 6	/note= "Gln(Trt)"
FT	Misc-difference 9	/note= "His(Trt)"
FT	Misc-difference 10	/note= "Asn(Trt)"
XX	W09952933-A1.	
PN	21-OCT-1999.	
XX	15-APR-1999;	99WO-US008435.
PF	15-APR-1998;	98US-0081897P.
XX	(RHON ) RHONE-POULENC RORER PHARM INC.	
PA	Sledeski AW, Mancel JJ;	
PI	WI; 1999-633822/54.	
DR	Convergent synthesis of peptides for treating e.g. bone disorders.	
XX	Disclosure; Page 75; 85pp; English.	
CC	This invention describes a novel method for the preparation of peptides (II) that contain both cyclic and linear peptide fragments comprises sequential reaction of a resin-bound linear fragment with the cyclic fragment in N-protected form and optionally other linear fragments. The products of the invention have osteopathic and hypotensive activity. (II) bind to hPTH receptors and act as agonists or antagonists of hPTH. The method is particularly used to prepare cyclic peptide analogs of parathyroid hormone (PTH) or PTH-related peptides which are useful for treating diseases that respond to treatment with agents that bind to PTH receptors (with or without activation of adenylyl cyclase activity), e.g. hyper- or hypo-calcaemia, osteoporosis, osteopenia, hyper- or hypo-parathyroidism, Cushing's syndrome, renal failure and hypertension, also for promoting repair of bone fractures. Separate synthesis of the cyclic fragment allows convergent synthesis of resin-bound (II), with better yields and higher throughput. The difficulties associated with preparation of the bridged fragment are confined to a small peptide which can be purified before reaction with the resin-bound component. AAY50568-Y50614 represent the peptide fragments described in the method of the invention	
XX	Sequence 11 AA;	
QY	Query Match 68.0%; Score 41.5; DB 2; Length 11; Best Local Similarity 83.3%; Pred. No. 0.5; Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;	
DQ	1 AVSEIOFMNLG 12       :      1 AVSEIO-LNVLG 11	
DE	Result 9 AAB86225 standard; peptide; 9 AA.	
ID	AAB86225 standard; peptide; 9 AA.	
AC	AAB86225;	
DT	03-SEP-2001 (first entry)	
XX	Human parathyroid hormone immunogenic peptide SEQ ID 7.	
XX	Parathyroid hormone; hPTH; immunogenic peptide; human; epitope; diagnosis; calcium-metabolism disorder; osteopathy; antagonist; hypo-parathyroidism; hyper-parathyroidism.	
OS	Homo sapiens.	
XX	20-OCT-1999;	99WO-US024481.
PF	20-OCT-1999;	99WO-US024481.
XX	21-JUN-2001.	
PD	17-DEC-1999;	99DE-01061350.
XX	17-DEC-1999;	99DE-01061350.
PR	(IMMU-) IMMUNDIAGNOSTIK AG.	
PA	Armbruster FP;	
PI	WI; 2001-376318/40.	
DR	Determining the content of physiologically active parathyroid hormone, useful in diagnosis of calcium-metabolism disorders, using two antibodies reactive with different epitopes.	
XX	Disclosure; Page 3; 10pp; German.	
CC	This invention describes a novel method for determining (M1) the content of active parathyroid hormone (A) by treating a sample with (i) antibody (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A), and including the N-terminal residue and (ii) antibody (Ab2) that recognizes an epitope within the receptor-binding site of (A). The number of molecules that react with both antibodies is determined and used to calculate the content of physiologically active (A). The method is used for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or hyper-parathyroidism. The method (unlike known assays) recognizes that (i) some fragments of (A) shorter than the complete (84 aa) peptide are active and (ii) that apparently intact peptide may be biologically inactive, and also takes into account the fact that some fragments of (A) are antagonistic (these have the receptor-binding site but lack the N-terminalus). It thus provides a true measure of the content of physiologically active (A); contrast methods that measure intact peptide and its 1-37 fragment which may produce falsely high values. This sequence represents a peptide fragment used to illustrate the method of the invention	
XX	Sequence 9 AA;	
QY	Query Match 67.2%; Score 41; DB 4; Length 9; Best Local Similarity 88.9%; Pred. No. 1.4e+06; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
DQ	2 VSEIOFMHN 10       :      1 VSEIQLMHN 9	
DE	Result 10 AAB01862 standard; peptide; 9 AA.	
ID	AAB01862 standard; peptide; 9 AA.	
AC	AAB01862;	
DT	11-SEP-2000 (first entry)	
XX	PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.	
XX	Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP; calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis; bone synthesis; agonist; osteoporosis; non-parenteral delivery.	
OS	Homo sapiens.	
XX	Synthetic.	
PN	W0200023594-A1.	
XX	27-APR-2000.	
PD	27-APR-2000.	
XX	20-OCT-1999;	99WO-US024481.
PF	20-OCT-1999;	99WO-US024481.

XX PR 22-OCT-1998; 98US-0105530P.  
 XX PA (GARD/) GARDELLA T J.  
 XX PA (KRON/) KRONENBERG H M.  
 XX PA (POTT/) POTTS J T.  
 XX PA (JUEP/) JUEPPNER H.  
 XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX DR WPI; 2000-339693/29.  
 XX PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 XX acids that encode them, useful for treating osteoporosis.  
 XX PS Disclosure; Page 26; 73pp; English.  
 XX CC The invention relates to a novel parathyroid hormone (PTH) peptide  
 CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal,  
 CC skeletal, neurological system, neuromuscular and cardiovascular systems.  
 CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
 CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterized by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodeling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists  
 XX Sequence 9 AA;  
 Query Match 63.9%; Score 39; DB 3; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AVSEIQFMH 9  
 Db 1 AVSEIQLMH 9  
 RESULT 11  
 ID AAY96966 standard; peptide; 9 AA.  
 XX AAY96966;  
 XX 31-OCT-2000 (first entry)  
 DT Parathyroid hormone N-terminal signaling domain (residues 1-9).  
 DE PTH; parathyroid hormone, N-terminal; signaling domain; bone mass;  
 KW

XX bone reformation; resorption; remodeling; tether1; osteoporosis.  
 XX Homo sapiens.  
 XX WO200039278-A2.  
 XX 06-JUL-2000.  
 XX 30-DEC-1999; 99WO-US031108.  
 XX 31-DEC-1998; 98US-0114577P.  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 XX (JUEP/) JUEPPNER H.  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-452384/39.  
 XX New compound comprising an amino terminal signaling functional domain  
 XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
 XX treating mammalian conditions characterized by decreases in bone mass.  
 XX Claim 4; Page 92; 119pp; English.  
 XX Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or S-(L)n  
 XX -R, are new. S is an amino terminal signaling functional domain of  
 XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
 XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R1 is the  
 XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 XX sequence. The new compounds are used for treating mammalian conditions  
 XX characterized by decreases in bone mass, determining rates of bone  
 XX reformation, bone resorption and/or bone remodeling, treating diseases  
 XX and disorders associated with decreased tether1 activity, increasing CAMP  
 XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 XX non-peptide PTH (claimed). The new compound can be administered by  
 XX inhalation unlike the large native PTH or PTHrP which avoids the need for  
 XX regular injections to treat osteoporosis  
 XX Sequence 9 AA;  
 Query Match 63.9%; Score 39; DB 3; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AVSEIQFMH 9  
 Db 1 AVSEIQLMH 9  
 RESULT 12  
 ID AAR91645 standard; peptide; 9 AA.  
 XX AAR91645;  
 XX 06-NOV-1996 (first entry)  
 DT Human parathyroid hormone antigenic peptide hPTH 1-9.  
 DE Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;  
 KW diagnosis; active hPTH 1-37.  
 XX Synthetic.  
 XX DE34434551-A1.  
 XX 04-APR-1996.  
 XX 28-SEP-1994; 94DE-04434551.

XX 28-SEP-1994; 94DE-04434551.  
 XX (FORS/) FORSMANN W.  
 XX Adermann K, Forssmann W, Hock D, Maegerlein M;  
 XX WPI; 1996-180391/19.  
 XX  
 XX New antigenic peptide(s) from human parathyroid hormone - and antibodies  
 XX generated using them, able to distinguish between active and inactive  
 XX forms of the hormone.  
 XX  
 XX Claim 2; Page 4; 5pp; German.  
 XX  
 XX The present sequence is a specific example of claimed immunogenic  
 XX peptides having a sequence from hPTH(1-37) which includes the N- or C-  
 XX terminal alpha-helical region and/or the non-structured region of the  
 XX hormone. Antibodies and their binding fragments generated by injecting an  
 XX animal with the peptides are useful as diagnostic reagents for  
 XX determination of biologically active hPTH(1-37)  
 XX  
 XX Sequence 9 AA;  
 XX Query Match 59.0%; Score 36; DB 2; Length 9;  
 XX Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AVSEIQFMH 9  
 XX :|||||:  
 XX 1 SVSEIQLMH 9  
 XX  
 XX  
 XX RESULT 13  
 XX ID AAB01863 standard; peptide; 9 AA.  
 XX AC AAB01863;  
 XX  
 XX 11-SEP-2000 (first entry)  
 XX  
 XX PTH(1-14) PTHrP(1-14)-derived peptide, SEQ ID NO:7.  
 XX  
 XX Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;  
 XX calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;  
 XX bone synthesis; agonist; osteoporosis; non-parenteral delivery.  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 XX  
 XX WO200023594-A1.  
 XX  
 XX 27-APR-2000.  
 XX  
 XX 20-OCT-1999; 99WO-US024481.  
 XX  
 XX 22-OCT-1998; 98US-0105530P.  
 XX  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 XX (JUEP/) JUEPPNER H.  
 XX  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-339693/29.  
 XX  
 XX Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic  
 XX acids that encode them, useful for treating osteoporosis.  
 XX  
 XX Disclosure; Page 26; 73pp; English.  
 XX  
 XX The invention relates to a novel parathyroid hormone (PTH) peptide

CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and  
 CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-  
 CC B01869). The peptides of the invention are at least 85% identical to the  
 CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Ileu-X3-His-X4-X5-  
 CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is  
 CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;  
 CC provided that the peptide is not PTHrP(1-14). The peptides of the  
 CC invention also encompass fragments of peptides of the invention  
 CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-  
 CC terminal derivatives. PTH is a major regulator of calcium homeostasis,  
 CC and is necessary for the normal function of the gastrointestinal, skeletal,  
 CC and is necessary for the normal function of the gastrointestinal, skeletal,  
 CC it binds to both PTH-1 receptors on osteoblasts and renal tubular cells,  
 CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic  
 CC effect on the skeleton, and mediates calcium reabsorption, enhances  
 CC phosphate clearance and vitamin D synthesis in the kidney. A homologous  
 CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of  
 CC the renal and skeletal actions of PTH, and also bind to the PTH-1  
 CC receptor. They do not bind to the PTH-2 receptor. The peptides of the  
 CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,  
 CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-  
 CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of  
 CC conditions characterised by a decrease in bone mass, such as  
 CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating  
 CC medical disorders that arise from excessive or altered action of the PTH-  
 CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also  
 CC useful in the determination of rates of bone formation, bone resorption  
 CC and/or bone remodelling in a patient. The peptides of the invention are  
 CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by  
 CC conventional synthetic chemistry, and can be delivered to a patient via  
 CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent  
 CC PTH-1/PTH-2 receptor agonists  
 XX  
 XX Sequence 9 AA;  
 XX Query Match 59.0%; Score 36; DB 3; Length 9;  
 XX Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 XX QY 1 AVSEIQFMH 9  
 XX :|||||:  
 XX 1 AVSEIQLMH 9  
 XX  
 XX  
 XX RESULT 14  
 XX AAY96981  
 XX ID AAY96981 standard; peptide; 9 AA.  
 XX AC AAY96981;  
 XX  
 XX 31-OCT-2000 (first entry)  
 XX  
 XX Parathyroid hormone N-terminal signaling domain.  
 XX  
 XX PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;  
 XX bone reformation; resorption; remodeling; tether1; osteoporosis.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2000039278-A2.  
 XX  
 XX 06-JUL-2000.  
 XX  
 XX 30-DEC-1999; 99WO-US031108.  
 XX  
 XX 31-DEC-1998; 98US-0114577P.  
 XX  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 XX (JUEP/) JUEPPNER H.  
 XX  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.  
 XX New compound comprising an amino terminal signaling functional domain  
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
 PT treating mammalian conditions characterized by decreases in bone mass.  
 XX Claim 11; Page 93; 119pp; English.  
 XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
 CC -R, are new, S is an amino terminal signaling functional domain of  
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where  
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R<sub>1</sub> is the  
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
 CC sequence. The new compounds are used for treating mammalian conditions  
 CC characterized by decreases in bone mass, determining rates of bone  
 CC reformation, bone resorption and/or bone remodeling, treating diseases  
 CC and disorders associated with decreased tethered activity, increasing cAMP  
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
 CC non-peptide PTH (claimed). The new compound can be administered by  
 CC inhalation unlike the large native PTH or PTHrp which avoids the need for  
 CC regular injections to treat osteoporosis  
 XX Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9  
 :|||||  
 Db 1 SVSEIQLMH 9

## RESULT 15

AAB86220  
 ID AAB86220 standard; peptide; 9 AA.

AC AAB86220;

DT 03-SEP-2001 (first entry)

DE Human parathyroid hormone immunogenic peptide SEQ ID 2.

KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;  
 KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;  
 KW hypo-parathyroidism; hyper-parathyroidism.

XX Homo sapiens.

PN DE19961350-A1.

XX 21-JUN-2001...

PF 17-DEC-1999; 99DE-01061350.

PR 17-DEC-1999; 99DE-01061350.

XX (IMMU-) IMMUNDIAGNOSTIK AG.

XX Armbruster PP;

XX WPI; 2001-376318/40.

XX Determining the content of physiologically active parathyroid hormone,  
 PT useful in diagnosis of calcium-metabolism disorders, using two antibodies  
 PT reactive with different epitopes.

PS Disclosure; Page 3; 10pp; German.

XX This invention describes a novel method for determining (M1) the content  
 CC of active parathyroid hormone (A) by treating a sample with (i) antibody

CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),  
 CC and including the N-terminal residue and (ii) antibody (Ab2) that  
 CC recognizes an epitope within the receptor-binding site of (A). The number  
 CC of molecules that react with both antibodies is determined and used to  
 CC calculate the content of physiologically active (A). The method is used  
 CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or  
 CC hyper-parathyroidism. The method (unlike known assays) recognizes that  
 CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are  
 CC active and (ii) that apparently intact peptide may be biologically  
 CC inactive, and also takes into account the fact that some fragments of (A)  
 CC are antagonistic (these have the receptor-binding site but lack the N-  
 CC terminus). It thus provides a true measure of the content of  
 CC physiologically active (A); contrast methods that measure intact peptide  
 CC and its 1-37 fragment which may produce falsely high values. This  
 CC sequence represents a peptide fragment used to illustrate the method of  
 CC the invention

XX Sequence 9 AA;

Query Match 59.0%; Score 36; DB 4; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9  
 :|||||  
 Db 1 SVSEIQLMH 9

Search completed: September 5, 2004, 09:34:31  
 Job time : 37.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds  
(without alignments)  
116.332 Million cell updates/sec

Title: US-09-730-174A-6  
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US02\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US03A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US03B\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	12	9	US-09-730-174A-6
2	58	95.1	12	9	US-09-730-174A-4
3	57	93.4	11	9	US-09-730-174A-2
4	55	90.2	12	9	US-09-730-174A-5
5	52	85.2	12	9	US-09-730-174A-3
6	51	83.6	11	9	US-09-730-174A-1
7	42	68.9	10	14	US-10-168-185-1
8	41	67.2	9	14	US-10-168-185-7
9	39	63.9	9	14	US-10-192-673-6
10	37	60.7	8	14	US-10-168-185-8
11	36	59.0	9	14	US-10-192-673-7
12	36	59.0	9	14	US-10-168-185-2
13	29	47.5	9	14	US-10-192-673-8
14	28	45.9	8	14	US-10-168-185-3
15	27	44.3	10	14	US-10-232-187-8

16	27	44.3	10	15	US-10-366-709-2	Sequence 2, Appli
17	26	42.6	9	14	US-10-192-673-10	Sequence 10, Appl
18	25	41.0	10	9	US-09-976-787-4	Sequence 4, Appli
19	25	41.0	10	9	US-09-865-198-4	Sequence 4, Appli
20	25	41.0	10	9	US-09-965-099-12	Sequence 12, Appl
21	25	41.0	10	10	US-09-563-222-41	Sequence 41, Appl
22	25	41.0	10	10	US-09-798-689-4	Sequence 4, Appli
23	25	41.0	10	12	US-10-239-656-19	Sequence 19, Appl
24	25	41.0	10	13	US-10-051-853-12	Sequence 12, Appl
25	25	41.0	10	14	US-10-195-753-108	Sequence 108, App
26	25	41.0	10	14	US-10-160-232-12	Sequence 12, Appl
27	25	41.0	10	14	US-10-160-232-18	Sequence 18, Appl
28	25	41.0	10	14	US-10-283-349-49	Sequence 49, Appl
29	25	41.0	10	14	US-10-230-880-115	Sequence 115, App
30	25	41.0	10	15	US-10-137-867-526	Sequence 526, App
31	25	41.0	10	15	US-10-366-709-3	Sequence 3, Appli
32	25	41.0	10	15	US-10-430-176-12	Sequence 12, Appl
33	25	41.0	11	11	US-09-791-551-13	Sequence 13, Appl
34	24	39.3	9	9	US-09-834-765-45	Sequence 45, Appl
35	24	39.3	9	9	US-09-834-765-55	Sequence 55, Appl
36	24	39.3	10	9	US-09-834-765-73	Sequence 73, Appl
37	24	39.3	10	9	US-09-910-059-26	Sequence 26, Appl
38	24	39.3	10	9	US-09-910-059-26	Sequence 61, Appl
39	24	39.3	10	14	US-10-033-741-61	Sequence 14, Appl
40	24	39.3	11	14	US-10-153-334-14	Sequence 93, Appl
41	24	39.3	11	16	US-10-391-364-93	Sequence 16, Appl
42	24	39.3	12	14	US-10-319-130-16	Sequence 5, Appli
43	23	37.7	6	14	US-10-168-185-5	Sequence 4, Appli
44	23	37.7	7	14	US-10-168-185-4	Sequence 508, App
45	23	37.7	8	14	US-10-043-487-508	

## ALIGNMENTS

## RESULT 1

US-09-730-174A-6  
; Sequence 6, Application US/09730174A  
; Patent No. US20020110871A1  
; GENERAL INFORMATION:  
; APPLICANT: Zahradnik, R.J.  
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H  
; FILE REFERENCE: IMUNE-001A  
; CURRENT APPLICATION NUMBER: US/09/730,174A  
; CURRENT FILING DATE: 2000-12-05  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 6  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies  
US-09-730-174A-6

Query Match 100.0%; Score 61; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQFMHNLG 12  
| | | | | | | | | |  
Db 1 AVSEIQFMHNLG 12

## RESULT 2

US-09-730-174A-4  
; Sequence 4, Application US/09730174A  
; Patent No. US20020110871A1  
; GENERAL INFORMATION:  
; APPLICANT: Zahradnik, R.J.  
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having  
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H  
; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 4  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-4

Query Match 95.1%; Score 58; DB 9; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.0049; Indels 0; Gaps 0;  
 Matches 11; Conservative 1; Mismatches 0;

QY 1 AVSEIQFMHNLG 12  
 :|||||  
 Db 1 SVSEIQFMHNLG 12

## RESULT 3

US-09-730-174A-2  
 ; Sequence 2, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 2  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-2

Query Match 93.4%; Score 57; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00068; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0;

QY 2 VSEIQFMHNLG 12  
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 Db 1 VSEIQFMHNLG 11

## RESULT 4

US-09-730-174A-5  
 ; Sequence 5, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 5  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-5

Query Match 90.2%; Score 55; DB 9; Length 12;  
 Best Local Similarity 91.7%; Pred. No. 0.0018; Indels 1; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 1;

QY 1 AVSEIQFMHNLG 12  
 :|||||  
 Db 1 AVSEIQFMHNLG 12

## RESULT 5

US-09-730-174A-3  
 ; Sequence 3, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 3  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-3

Query Match 85.2%; Score 52; DB 9; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 0.0063; Indels 1; Gaps 0;  
 Matches 10; Conservative 1; Mismatches 1;

QY 1 AVSEIQFMHNLG 12  
 :|||||  
 Db 1 SVSEIQFMHNLG 12

## RESULT 6

US-09-730-174A-1  
 ; Sequence 1, Application US/09730174A  
 ; Patent No. US20020110871A1  
 ; GENERAL INFORMATION:

; APPLICANT: Zahradnik, R.J.  
 ; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a  
 ; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho  
 ; FILE REFERENCE: IMUNE-001A  
 ; CURRENT APPLICATION NUMBER: US/09/730,174A  
 ; CURRENT FILING DATE: 2000-12-05  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SEQ ID NO 1  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies

US-09-730-174A-1

Query Match 83.6%; Score 51; DB 9; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.0089; Indels 1; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 1;

QY 2 VSEIQFMHNLG 12  
 :|||||  
 Db 1 VSEIQFMHNLG 11

## RESULT 7

US-10-168-185-1  
 ; Sequence 1, Application US/10168185  
 ; Publication No. US20030175802A1  
 ; GENERAL INFORMATION:

; APPLICANT: Armbruster, Franz Paul  
 ; APPLICANT: Misbachler, Albert  
 ; APPLICANT: Schmidt-Gayk, Heinrich  
 ; APPLICANT: Roth, Heinz-Jurgen  
 ; TITLE OF INVENTION: Method for Determining Parathormone

```

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-1

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Query Match      68.9%; Score 42; DB 14; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.38;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

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QY 1 AVSEIQFMEN 10
    ||||| |||
DB 1 SVSEIQLMEN 10

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RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-7

```

```

Query Match      67.2%; Score 41; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 VSEIQFMEN 10
    ||||| |||
DB 1 VSEIQLMEN 9

```

```

RESULT 9
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)
; FILE REFERENCE: 0609.4570002

```

```

; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-192-673-6

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Query Match      63.9%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AVSEIQFMH 9
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DB 1 AVSEIQLMH 9

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RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-8

```

```

Query Match      60.7%; Score 37; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3 SEIQFMHN 10
    ||||| |||
DB 1 SEIQLMHN 8

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RESULT 11
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)

```

us-09-730-174a-6.closed.rapb

Sun Sep 5 09:56:58 2004

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; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-10-192-673-7

```

```

Query Match          59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 AVSEIQFMH 9
   |||||
Db 1 AVSEIQLMH 9

```

```

RESULT 12
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-185-2

```

```

Query Match          59.0%; Score 36; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 AVSEIQFMH 9
   :|||
Db 1 SVSEIQLMH 9

```

```

RESULT 13
US-10-192-673-8
; Sequence 8, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid

```

```

; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: U.S. 60/105,530
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-10-192-673-8

```

```

Query Match          47.5%; Score 29; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 AVSEIQFMH 9
   |||||
Db 1 AVSEHQLH 9

```

```

RESULT 14
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jürgen
; TITLE OF INVENTION: Method for Determining Parathormone
; FILE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-168-185-3

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Query Match          45.9%; Score 28; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AVSEIQFM 8
   :|||
Db 1 SVSEIQLM 8

```

```

RESULT 15
US-10-232-187-8
; Sequence 8, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert

```

; APPLICANT: Nulku, Turkan E.  
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies  
; FILE REFERENCE: GH50042-1  
; CURRENT APPLICATION NUMBER: US/10/232,187  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/187,595  
; PRIOR FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: PCT/US01/07193  
; PRIOR FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/315,943  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/349,830  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: 60/394,741  
; PRIOR FILING DATE: 2002-07-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-232-187-8

Query Match 44.3%; Score 27; DB 14; Length 10;  
Best Local Similarity 44.4%; Pred. No. 2 3e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 AVSEIQFMH 9  
Db 2 ATSSVSYMH 10

Search completed: September 5, 2004, 09:49:38  
Job time : 32.5 secs

This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:32:03 ; Search time 11 Seconds  
(without alignments)  
56.319 Million cell updates/sec

Title: US-09-730-174A-6  
Perfect score: 61  
Sequence: 1 AVSEIQPHNLG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pap.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pap.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pap.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pap.\*  
5: /cgn2\_6/ptodata/2/iaa/PTCUS COMB.pap.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	80.3	12	4	US-09-442-989-31
2	42	68.9	10	3	US-08-817-547A-1
3	39	63.9	9	4	US-09-421-379-6
4	36	59.0	9	3	US-08-817-547A-2
5	36	59.0	9	4	US-09-421-379-7
6	31	50.8	11	6	5460978-3
7	29	47.5	9	4	US-09-421-379-8
8	29	47.5	12	2	US-08-140-137A-42
9	28	45.9	12	3	US-08-817-547A-3
10	27	44.3	12	2	US-08-482-228-42
11	27	44.3	12	3	US-08-482-528-42
12	26	42.6	9	4	US-09-421-379-10
13	25	41.0	10	2	US-08-116-778E-9
14	25	41.0	10	2	US-08-438-562-9
15	25	41.0	10	2	US-08-483-528B-97
16	25	41.0	10	3	US-08-783-853A-12
17	25	41.0	10	3	US-08-836-561-49
18	25	41.0	10	3	US-09-280-028-12
19	25	41.0	10	4	US-09-344-050-12
20	25	41.0	10	4	US-09-393-385B-108
21	25	41.0	10	4	US-09-434-122-49
22	25	41.0	10	4	US-09-091-071-3
23	24	39.3	5	2	US-08-177-109A-56
24	24	39.3	5	2	US-08-687-706-56
25	24	39.3	5	3	US-08-817-547A-17
26	24	39.3	6	3	US-08-817-547A-16
27	24	39.3	7	3	US-08-817-547A-15

# ALIGNMENTS

## RESULT 1

US-09-442-989-31

; Sequence 31, Application US/09442989

; Patent No. 6569993

; GENERAL INFORMATION:

; APPLICANT: Sledeski, Adam W.

; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC

; FILE REFERENCE: A3113B-US

; CURRENT APPLICATION NUMBER: US/09/442,989

; CURRENT FILING DATE: 1999-11-18

; EARLIER APPLICATION NUMBER: 60/081,897

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 31

; TYPE: PRT

; LENGTH: 12

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)

; OTHER INFORMATION: FMOC-Ala

; NAME/KEY: PEPTIDE

; LOCATION: (3)

; OTHER INFORMATION: Ser (OtBu)

; NAME/KEY: PEPTIDE

; LOCATION: (4)

; OTHER INFORMATION: Glu (OtBu)

; NAME/KEY: PEPTIDE

; LOCATION: (6)

; OTHER INFORMATION: Gln (Trt)

; NAME/KEY: PEPTIDE

; LOCATION: (9)

; OTHER INFORMATION: His (Trt)

; NAME/KEY: PEPTIDE

; LOCATION: (10)

; OTHER INFORMATION: Asn (Trt)

; NAME/KEY: MOD RES

; LOCATION: (8)

; OTHER INFORMATION: Nle

; US-09-442-989-31

Sequence 64, Appl  
Sequence 14, Appl  
Sequence 64, Appl  
Sequence 13, Appl  
Sequence 5, Appl  
Sequence 7, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 5, Appl  
Sequence 4, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 83, Appl

24 39.3 8 2 US-08-748-021-64  
24 39.3 8 3 US-08-817-547A-14  
24 39.3 8 3 US-08-974-297-64  
24 39.3 9 3 US-08-817-547A-13  
24 39.3 10 1 US-08-432-694-5  
24 39.3 10 3 US-08-817-547A-7  
24 39.3 10 3 US-09-171-945-26  
24 39.3 11 1 US-08-432-694-3  
23 37.7 6 3 US-08-817-547A-5  
23 37.7 7 3 US-08-817-547A-4  
23 37.7 9 1 US-07-822-043-26  
23 37.7 9 1 US-08-346-455B-26  
23 37.7 9 3 US-08-977-221-26  
23 37.7 9 4 US-09-483-831B-26  
23 37.7 9 5 PCT-US95-06613-26  
23 37.7 10 4 US-09-771-415-3  
23 37.7 12 3 US-09-064-750-1  
22 36.1 10 1 US-08-615-181-83

Query Match 80.3%; Score 49; DB 4; Length 12;  
Best Local Similarity 83.3%; Pred. No. 0.0034;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQFMHNLG 12  
Db 1 AVSEIQFMHNLG 12

RESULT 2  
US-08-817-547A-1

; Sequence 1, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A

; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03757  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: no  
; ANTI-SENSE: no

US-08-817-547A-1

Query Match 68.9%; Score 42; DB 3; Length 10;  
Best Local Similarity 80.0%; Pred. No. 0.06;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMHN 10  
Db 1 SVSEIQFMHN 10

RESULT 3

US-09-421-379-6

; Sequence 6, Application US/09421379  
; Patent No. 6495662  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: Kronenberg, Henry  
; APPLICANT: Potts, John T.  
; APPLICANT: Juppner, Harald

; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
; FILE REFERENCE: 0609.4570001  
; CURRENT APPLICATION NUMBER: US/09/421,379  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: U.S. 60/105,530  
; EARLIER FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PPT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-421-379-6

Query Match 63.9%; Score 39; DB 4; Length 9;  
Best Local Similarity 88.9%; Pred. No. 3e+05;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9  
Db 1 AVSEIQFMH 9

RESULT 4

US-08-817-547A-2

; Sequence 2, Application US/08817547A  
; Patent No. 6030790  
; GENERAL INFORMATION:  
; APPLICANT: Adermann, Knut  
; APPLICANT: Hock, Dieter  
; APPLICANT: Magerlein, Markus  
; TITLE OF INVENTION: Peptides from the hPTH Sequence  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jones & Askew, LLP  
; STREET: 191 Peachtree Street, 37th Floor  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,547A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/03757  
; FILING DATE: 29 SEPT 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FROST, ROGER T.  
; REGISTRATION NUMBER: 22,176  
; REFERENCE/DOCKET NUMBER: 07826-0007  
; TELEPHONE: 404-818-3700  
; TELEFAX: 404-818-3799

; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
US-08-817-547A-2

Query Match 59.0%; Score 36; DB 3; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 3e+05;  
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 AVSEIQFMH 9  
 :|||||  
 Db 1 SVSEIQLMH 9

RESULT 5  
 US-09-421-379-7  
 ; Sequence 7, Application US/09421379  
 ; Patent No. 6495662  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gardella, Thomas J.  
 ; APPLICANT: Kronenberg, Henry  
 ; APPLICANT: Potts, John T.  
 ; APPLICANT: Juppner, Harald  
 ; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
 ; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
 ; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
 ; FILE REFERENCE: 0609.4570001  
 ; CURRENT APPLICATION NUMBER: US/09/421,379  
 ; CURRENT FILING DATE: 1999-10-20  
 ; EARLIER APPLICATION NUMBER: U.S. 60/105,530  
 ; EARLIER FILING DATE: 1998-10-22  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-421-379-7

Query Match 59.0%; Score 36; DB 4; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 3e+05;  
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 AVSEIQFMH 9  
 :|||||  
 Db 1 AVSEIQLH 9

RESULT 6  
 5460978-3  
 ; Patent No. 5460978  
 ; APPLICANT: MARTIN, THOMAS J.; MOSELEY, JANE M.; KEMP,  
 ; BRUCE E.; WETTENHALL, RICHARD E.H.  
 ; TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL  
 ; HYPERCALCAEMIA OF MALIGNANCY-PTHRP  
 ; NUMBER OF SEQUENCES: 4  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/715,280  
 ; FILING DATE: 14-JUN-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 199,235  
 ; FILING DATE: 09-MAY-1988  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; SEQ ID NO:3  
 ; LENGTH: 11  
 5460978-3

Query Match 50.8%; Score 31; DB 6; Length 11;  
 Best Local Similarity 70.0%; Pred. No. 8.5;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 10  
 :|||||

Db 1 AVSEHQLHN 10

RESULT 7  
 US-09-421-379-8  
 ; Sequence 8, Application US/09421379  
 ; Patent No. 6495662  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gardella, Thomas J.  
 ; APPLICANT: Kronenberg, Henry  
 ; APPLICANT: Potts, John T.  
 ; APPLICANT: Juppner, Harald  
 ; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
 ; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
 ; TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
 ; FILE REFERENCE: 0609.4570001  
 ; CURRENT APPLICATION NUMBER: US/09/421,379  
 ; CURRENT FILING DATE: 1999-10-20  
 ; EARLIER APPLICATION NUMBER: U.S. 60/105,530  
 ; EARLIER FILING DATE: 1998-10-22  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-421-379-8

Query Match 47.5%; Score 29; DB 4; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 3e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9  
 :|||||  
 Db 1 AVSEHQLH 9

RESULT 8  
 US-08-140-137A-42  
 ; Sequence 42, Application US/08140137A  
 ; Patent No. 5817617  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TUOMANEN, ELAINE  
 ; APPLICANT: MASURE, H. R.  
 ; TITLE OF INVENTION: ANALOGS OF ENDOTHELIAL LEUKOCYTE  
 ; TITLE OF INVENTION: ADHESION MOLECULE (ELAM)  
 ; NUMBER OF SEQUENCES: 49  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Klauber & Jackson  
 ; STREET: 411 Hackensack Avenue  
 ; CITY: Hackensack  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/140,137A  
 ; FILING DATE: 27-MAY-1994  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Jackson Esq., David A.  
 ; REGISTRATION NUMBER: 26,742  
 ; REFERENCE/DOCKET NUMBER: 600-1-096  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201 487-5800  
 ; TELEFAX: 201 343-1684

us-09-730-174a-6.closed.ra1

Sun Sep 5 09:56:58 2004

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; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: CARD peptide sequence
; US-08-140-137A-42

Query Match 47.5%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQFMH 9
Db 5 ISEEQFVH 12

RESULT 9
US-08-817-547A-3
; Sequence 3, Application US/08817547A
; Patent No. 6030790
; GENERAL INFORMATION:
; APPLICANT: Adermann, Knut
; APPLICANT: Hock, Dieter
; APPLICANT: Magerlein, Markus
; TITLE OF INVENTION: Peptides from the hPTH Sequence
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,547A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/03757
; FILING DATE: 29 SEPT 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROST, ROGER T.
; REGISTRATION NUMBER: 22,176
; REFERENCE/DOCKET NUMBER: 07826-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-817-547A-3

Query Match 45.9%; Score 28; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVSEIQFM 8
Db 1 SVSEIQFM 8

; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: CARD peptide sequence
; US-08-140-137A-42

Query Match 44.3%; Score 27; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
Db 3 ASSSVTFMH 11

RESULT 11
US-08-482-528-42
; Sequence 42, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-228-42

Query Match 44.3%; Score 27; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AVSEIQFMH 9
Db 3 ASSSVTFMH 11

RESULT 11
US-08-482-528-42
; Sequence 42, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine

```

STATE: California  
COUNTRY: USA  
ZIP: 92713-5210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/482,528  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Guthrie, Janice  
REGISTRATION NUMBER: 35,170  
REFERENCE/DOCKET NUMBER: IT-4630CIP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 440-5353  
TELEFAX: (714) 553-1952  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-528-42

Query Match 44.3%; Score 27; DB 3; Length 12;  
Best Local Similarity 55.6%; Pred. No. 54;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9  
Db 3 ASSVTFMH 11

## RESULT 12

US-09-421-379-10  
Sequence 10, Application US/09421379  
Patent No. 6495662  
GENERAL INFORMATION:

APPLICANT: Gardella, Thomas J.  
APPLICANT: Kronenberg, Henry  
APPLICANT: Potts, John T.  
APPLICANT: Juppner, Harald  
TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of  
TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid  
TITLE OF INVENTION: Hormone-Related Peptide (PTHrp)  
FILE REFERENCE: 0609.4570001  
CURRENT APPLICATION NUMBER: US/09/421,379  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: U.S. 60/105,530  
EARLIER FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 10  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: Peptide

## US-09-421-379-10

Query Match 42.6%; Score 26; DB 4; Length 9;  
Best Local Similarity 55.6%; Pred. No. 3e+05;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9  
Db 1 SVSEHQLLH 9

## RESULT 13

US-08-116-778E-9  
Sequence 9, Application US/08116778E  
Patent No. 5830470  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,778E  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-59  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-116-778E-9

Query Match 41.0%; Score 25; DB 2; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9  
Db 2 ASSSVSYMH 10

## RESULT 14

US-08-438-562-9  
Sequence 9, Application US/08438562  
Patent No. 5874255  
GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KUWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

RESULT 15  
US-08-483-528B-97  
; Sequence 97, Application US/08483528B  
; Patent No. 5939532  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUMANA, YOSHIIISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,528B  
; FILING DATE: 07-JUN-95  
; CLASSIFICATION: 536  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid